

OM protein - protein search, using sw model

Run on: November 28, 2003, 14:24:03 ; Search time 41 Seconds  
(without alignments)  
19.357 Million cell updates/sec

Title: US-09-228-866-45  
Perfect score: 5  
Sequence: 1 XSRLX 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 408126

Minimum DB seq length: 5  
Maximum DB seq length: 23

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03:\*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*
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- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\*
- 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*
- 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*
- 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*
- 12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*
- 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\*
- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:\*
- 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\*
- 18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:\*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3	60.0	5	17	AAY16472	Cyclic thrombin re	
2	3	60.0	5	18	AAW12483	Interleukin-6 anta	
3	3	60.0	5	20	AAW94152	BC loop sequence o	
4	3	60.0	5	21	AAB11575	SEN virus epitope	
5	3	60.0	5	21	AAY83307	Peptide motif of S	
6	3	60.0	5	22	AAE03440	Human gene 14 enco	
7	3	60.0	5	22	AAE03489	Human gene 14 enco	
8	3	60.0	5	22	AAB49812	Human endostatin p	
9	3	60.0	5	23	AAE28216	Tobacco mosaic vir	
10	3	60.0	5	23	ABG63387	Human albumin fusi	
11	3	60.0	5	23	ABG63388	Human albumin fusi	
12	3	60.0	5	23	ABB94397	Ubiquitin binding	
13	3	60.0	5	23	ABB94451	Ubiquitin binding	
14	3	60.0	5	23	AAE19260	Human recombinant	
15	3	60.0	5	24	ABP55341	Cucurbita sp. pept	
16	3	60.0	6	17	AAY16474	Cyclic thrombin re	
17	3	60.0	6	18	AAW26814	Hexapeptide epitop	
18	3	60.0	6	19	AAY20645	Human neurofilamen	
19	3	60.0	6	19	AAW75318	Hexapeptide #11 bi	
20	3	60.0	6	19	AAW75386	Hexapeptide #11 bi	
21	3	60.0	6	20	AAY55284	ATCC HB 11885 mono	
22	3	60.0	6	21	AAY87030	Human haematopoiet	
23	3	60.0	6	21	AAY43709	Sequence of the se	
24	3	60.0	6	21	AAY43740	Sequence of the se	
25	3	60.0	6	22	AAM97492	Human peptide #767	
26	3	60.0	6	22	AAB49814	Human endostatin p	
27	3	60.0	6	22	AAB49815	Human endostatin p	
28	3	60.0	6	23	ABG60376	Selective targetin	
29	3	60.0	7	3	AAP20402	Secretin precursor	
30	3	60.0	7	4	AAP30020	Intermediate of se	
31	3	60.0	7	18	AAW11186	Brain homing pepti	
32	3	60.0	7	18	AAW27419	CDR2 from light ch	
33	3	60.0	7	20	AAY48768	Membrane dipeptida	
34	3	60.0	7	20	AAY48912	Membrane dipeptida	
35	3	60.0	7	20	AAY16941	Heat shock protein	
36	3	60.0	7	20	AAY05017	Tumour antigen ant	
37	3	60.0	7	20	AAY05021	Tumour antigen ant	
38	3	60.0	7	21	AAB28344	Neuropeptide NPFII	
39	3	60.0	7	21	AAB36149	Neuropeptide NPFII	
40	3	60.0	7	21	AAB26822	Peptidic membrane	
41	3	60.0	7	21	AAB17236	SH3 antagonist pep	
42	3	60.0	7	21	AAB12005	Brain homing pepti	
43	3	60.0	7	21	AAY94221	Murine 16E10 light	
44	3	60.0	7	22	AAU72083	Melanoma antigen,	
45	3	60.0	7	22	AAE11811	Phage peptide #19	
46	3	60.0	7	22	AAG63615	Complementarity de	
47	3	60.0	7	22	AAG63621	Complementarity de	
48	3	60.0	7	22	AAG98766	Human cell death p	
49	3	60.0	7	22	AAB84974	Clone 2 scFv CDR L	
50	3	60.0	7	22	AAB84986	G12 scFv CDR L2 re	

51	3	60.0	7	22	AAB30666	Neuropeptide F (NP
52	3	60.0	7	22	AAB49817	Human endostatin p
53	3	60.0	7	22	AAB49818	Human endostatin p
54	3	60.0	7	22	AAB49819	Human endostatin p
55	3	60.0	7	23	ABP66477	Human RSV antibody
56	3	60.0	7	23	ABP49256	Zinc finger protei
57	3	60.0	7	23	ABB73229	Src homology3 (SH3
58	3	60.0	7	23	AAU80633	Javelin peptide #6
59	3	60.0	7	23	AAU10722	Brain homing pepti
60	3	60.0	7	23	AAU11497	PAdV terminal prot
61	3	60.0	7	23	AAU11498	PAdV-5 terminal pr
62	3	60.0	7	23	AAU70359	Mouse Kappa V ligh
63	3	60.0	7	24	ABU69340	Respiratory syncyt
64	3	60.0	7	24	ABP56502	S. pneumoniae PPS-
65	3	60.0	8	15	AAR59433	Gp2b(896-903) pept
66	3	60.0	8	15	AAR48371	Peptide fragment w
67	3	60.0	8	15	AAR58622	GP2b residues 896-
68	3	60.0	8	15	AAR66119	Peptide derived fr
69	3	60.0	8	16	AAR79529	Anti-human chorion
70	3	60.0	8	17	AAR91288	Anti-idiotypic T-c
71	3	60.0	8	17	AAR90406	Hybridoma ATCC HB-
72	3	60.0	8	18	AAW26811	Octapeptide epitop
73	3	60.0	8	18	AAW26812	Octapeptide epitop
74	3	60.0	8	18	AAW26818	Hepatitis C virus
75	3	60.0	8	18	AAW26807	Octapeptide epitop
76	3	60.0	8	18	AAW26808	Octapeptide epitop
77	3	60.0	8	18	AAW26809	Octapeptide epitop
78	3	60.0	8	18	AAW26810	Octapeptide epitop
79	3	60.0	8	18	AAW10754	Binding peptide #1
80	3	60.0	8	19	AAW57524	Molecular mimetic
81	3	60.0	8	20	AAY32116	Maize id gene null
82	3	60.0	8	20	AAY53393	HIV-1 nef protein
83	3	60.0	8	20	AAY53467	HIV-1 nef protein
84	3	60.0	8	20	AAY55133	ATCC HB 11885 mono
85	3	60.0	8	20	AAY40242	Amino acid sequenc
86	3	60.0	8	20	AAY40316	Amino acid sequenc
87	3	60.0	8	20	AAY26734	HIV-derived lipope
88	3	60.0	8	20	AAY26808	HIV-derived lipope
89	3	60.0	8	20	AAY00373	Fragment of human
90	3	60.0	8	20	AAW67658	LXXLL signature mo
91	3	60.0	8	21	AAY86587	Telomerase peptide
92	3	60.0	8	21	AAY86879	Human haematopoiet
93	3	60.0	8	22	AAG77882	Human C35 peptide
94	3	60.0	8	22	ABB12719	Human C35 peptide
95	3	60.0	8	22	ABB12721	Human C35 peptide
96	3	60.0	8	22	ABB13695	Human C35 peptide
97	3	60.0	8	22	ABB13715	Human C35 peptide
98	3	60.0	8	22	ABB14655	Human C35 peptide
99	3	60.0	8	22	AAE12847	Human growth hormo
100	3	60.0	8	22	AAE12850	Human growth hormo

#### ALIGNMENTS

RESULT 1  
AAY16472

ID AAY16472 standard; peptide; 5 AA.  
XX  
AC AAY16472;  
XX  
DT 06-AUG-1999 (first entry)  
XX  
DE Cyclic thrombin receptor peptide analogue.  
XX  
KW Peptide analogue; N-terminal domain; cancer; angiogenesis; metastasis;  
KW human G protein linked thrombin receptor; cyclic; antagonist; agonist;  
KW cardiovascular disease; inflammatory disease; gastrointestinal disease;  
KW osteoporosis; tissue injury; tissue repair; nerve regeneration;  
KW thrombin-mimetic study; platelet function; myocardial infarction;  
KW arterial plaque formation.  
XX  
OS Synthetic.  
XX  
PN US5516889-A.  
XX  
PD 14-MAY-1996.  
XX  
PF 17-MAR-1995; 95US-0405933.  
XX  
PR 21-JUN-1993; 93US-0080643.  
PR 17-MAR-1995; 95US-0405933.  
XX  
PA (UYTE-) UNIV TECHNOLOGIES INT INC.  
XX  
PI Hollenberg MD, Matsoukas JM, Moore GJ;  
XX  
DR WPI; 1996-251084/25.  
XX  
PT New cyclic peptide(s) derived from the protein G linked thrombin  
PT receptor - are agonists or antagonists for treating diseases  
PT involving this receptor, e.g. myocardial infarction  
XX  
PS Disclosure; Column 33; 36pp; English.  
XX  
CC AAY16465-98 represent peptide analogues of the N-terminal domain of  
CC the human G protein linked thrombin receptor sequence. The peptides,  
CC which may be cyclic, have the formula X1-Psi-X2-X3-Omega-X4 in which  
CC Psi = any (non-)natural aromatic amino acid (aa); Omega = any  
CC (non-)natural basic aa or derivatives; X1 is absent or is a natural  
CC aa, 1-3C acyl or 1-5C alkyl; X2 = any natural aa; X3 is absent or is  
CC any natural aa; and X4 is absent or is any natural aa. The peptides  
CC are are antagonists and agonists for treating disorders involving  
CC thrombin receptors, e.g. cardiovascular, inflammatory or  
CC gastrointestinal diseases; osteoporosis; tissue injury and repair  
CC (including nerve regeneration); and cancer (by inhibiting angiogenesis  
CC and metastasis). They may also be used diagnostically and in  
CC thrombin-mimetic studies. The peptide analogues are particularly used to  
CC modulate platelet function (acting synergistically with aspirin-type  
CC compounds) and so are useful in cases of myocardial infarction, as well  
CC as to coat prostheses and to reduce arterial plaque formation.  
XX  
SQ Sequence 5 AA;



Query Match 60.0%; Score 3; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 1 SRL 3

RESULT 2

AAW12483

ID AAW12483 standard; peptide; 5 AA.

XX

AC AAW12483;

XX

DT 22-APR-1997 (first entry)

XX

DE Interleukin-6 antagonist 48.

XX

KW Interleukin-6; IL-6; antagonist; inhibitor; autoimmune disease;  
KW skin; intestine; systemic lupus erythematosus; chronic rheumatism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 5

FT /note= "amidated"

XX

PN JP08311098-A.

XX

PD 26-NOV-1996.

XX

PF 22-MAY-1995; 95JP-0146742.

XX

PR 22-MAY-1995; 95JP-0146742.

XX

PA (DAIL ) DAICEL CHEM IND LTD.

PA (FUJI ) FUJISAWA PHARM CO LTD.

XX

DR WPI; 1997-061811/06.

XX

PT Interleukin-6 antagonistic peptide(s) comprising arginine - useful  
PT for treating autoimmune, renal, skin and intestinal diseases

XX

PS Example 48; Page 12; 20pp; Japanese.

XX

CC The present peptide is a specific example of new interleukin-6  
CC antagonists of the general formula X-A-B-D-Y, where X is 1-10 amino  
CC acids or an amino group protecting group; Y is 1-5 amino acids, a  
CC carboxyl group protecting group or an amide; A is preferably Arg  
CC having an opt. protected guanidino group but can be any amino acid;  
CC D is Arg having an opt. protected guanidino group and B is preferably  
CC a Leu residue but can be any amino acid, including non-natural  
CC amino acids, opt. having a protected side-chain. The peptides are  
CC useful for treating autoimmune diseases (e.g. systemic lupus  
CC erythematosus or chronic rheumatism), renal, skin and intestinal  
CC diseases.

XX

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 18; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4

|||

Db 2 SRL 4

### RESULT 3

AAW94152

ID AAW94152 standard; peptide; 5 AA.

XX

AC AAW94152;

XX

DT 14-APR-1999 (first entry)

XX

DE BC loop sequence of ubiquitin-binding monobody clone 411.

XX

KW Fibronectin type III; Fn3; monobody; beta-strand domain; loop region;  
KW specific binding partner; SBP; catalysis; LRS; ubiquitin.

XX

OS Saccharomyces cerevisiae.

XX

PN W09856915-A2.

XX

PD 17-DEC-1998.

XX

PF 12-JUN-1998; 98WO-US12099.

XX

PR 12-JUN-1997; 97US-0049410.

XX

PA (RESE ) RESEARCH CORP TECHNOLOGIES INC.

XX

PI Koide S;

XX

DR WPI; 1999-060331/05.

XX

PT Production of antibody compounds, particularly catalytic antibodies

PT - using a fibronectin type III molecular scaffolding comprising

PT beta-strand domain sequences and modified in one or more loop

PT sequences

XX

PS Example 10; Page 41; 96pp; English.

XX

CC The invention relates to a synthetic fibronectin type III (Fn3)

CC polypeptide monobody that comprises Fn3 beta-strand domain sequences

CC that are linked to loop region sequences (LRSs). One or more of the loop

CC sequences in the synthetic Fn3 vary by deletion, insertion, or

CC replacement of at least 2 amino acids from the corresponding LRss in

CC wild-type Fn3. Host cells containing an expression vector comprising the

CC synthetic Fn3 nucleic acid are used for the production of the Fn3

CC monobody. The invention also provides methods of identifying the amino

CC acid sequence of a polypeptide molecule (i) capable of binding to a

CC specific binding partner (SBP) so as to form a polypeptide:SBP complex;  
CC (ii) capable of catalysing a chemical reaction with a catalysed rate  
CC constant, Kcat, and an uncatalysed rate constant, Kuncat, such that the  
CC ratio of the Kcat/kuncat is greater than 10. Sequences AAW94147-54  
CC represent BC loop sequences of yeast ubiquitin-binding monobodies.

XX

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 1 SRL 3

#### RESULT 4

AAB11575

ID AAB11575 standard; Peptide; 5 AA.

XX

AC AAB11575;

XX

DT 12-OCT-2000 (first entry)

XX

DE SEN virus epitope mapping peptide SEQ ID NO: 165.

XX

KW SEN virus; SENV; gastrointestinal tract disorder; inflammatory disease;  
KW proliferative disorder; hepatopathy; hepatitis; viral infection;  
KW vaccination; gene therapy.

XX

OS Hepatitis virus.

XX

PN WO200028039-A2.

XX

PD 18-MAY-2000.

XX

PF 09-NOV-1999; 99WO-EP08566.

XX

PR 10-NOV-1998; 98IT-MI02437.

PR 30-APR-1999; 99IT-MI00923.

PR 14-MAY-1999; 99EP-0830298.

PR 16-JUL-1999; 99EP-0113932.

XX

PA (DIAS-) DIASORIN SRL.

XX

PI Primi D, Fiordalisi G, Mantero GL, Mattioli S, Sottini A;

PI Bonelli F, Vaglini L, Olivero P, Dal Corso A, Bonelli M;

XX

DR WPI; 2000-376551/32.

XX

PT Nucleic acids representing the genome of the SEN virus (SENV) and  
PT encoded proteins, useful for treatment of hepatopathies, inflammatory  
PT diseases and proliferative disorders such as cancer -

XX

PS Example 28; Page 104; 392pp; English.

XX

CC The present invention is concerned with the sequence of the genome of  
CC the SENV virus (SENV), and the proteins encoded by it. SENV is thought to  
CC be the cause of hepatopathies which are not linked to the presence of  
CC the hepatitis A, B and E viruses in man. The genome and proteins of this  
CC virus can be used in gene therapy and vaccination against the virus,  
CC which also causes disorders of the gastrointestinal tract, including  
CC Crohn's disease and lupus erythematosus, inflammatory diseases, and  
CC proliferative disorders such as cancer. The peptides AAB11549-B11581  
CC were used in epitope mapping assays to identify the immunologically  
CC reactive areas of the SENV proteins.

XX

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 1 SRL 3

#### RESULT 5

AAY83307

ID AAY83307 standard; Peptide; 5 AA.

XX

AC AAY83307;

XX

DT 16-AUG-2000 (first entry)

XX

DE Peptide motif of SDD1 subtilisin-like serine protease.

XX

KW SDD1; serine protease; subtilisin; transgenic plants; dry weight;  
KW stomata; sugar; water; protein; CO<sub>2</sub>; H<sub>2</sub>O; CO<sub>2</sub>; H<sub>2</sub>O;  
KW crop protection; feed; foodstuffs.

XX

OS Synthetic.

OS Arabidopsis thaliana.

XX

PN WO200022144-A2.

XX

PD 20-APR-2000.

XX

PF 12-OCT-1999; 99WO-EP07633.

XX

PR 12-OCT-1998; 98EP-0119244.

XX

PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PA (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.

XX

PI Berger D, Altmann T;

XX

DR WPI; 2000-317995/27.

XX

PT Novel recombinant DNA molecules encoding subtilisin-like serine  
PT protease, useful for producing transgenic plants with altered stomata,  
PT lower water consumption and enhanced diseased resistance

XX  
 PS Disclosure; Page 9; 101pp; English.  
 XX  
 CC Sequences encoding SDD1, a subtilisin-like serine protease, can be  
 CC used to produce transgenic plants with altered stomata  
 CC characterisitics. These plants exhibit improved freshness,  
 CC increased dry weight, reduced leaf temperatures, reduced water loss  
 CC and lower water consumption and for enhancing the sugar and/or  
 CC protein content of plant leaves, modulating CO<sub>2</sub> uptake into and H<sub>2</sub>O  
 CC release from leaves, for sustained photosynthesis under high  
 CC intensity conditions or for the improvement of disease resistance  
 CC of plants. The transgenic plants and cells of such plants are useful  
 CC in the preparation of feed, food or additives.  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 2 SRL 4

RESULT 6  
 AAE03440  
 ID AAE03440 standard; peptide; 5 AA.  
 XX  
 AC AAE03440;  
 XX  
 DT 10-AUG-2001 (first entry)  
 XX  
 DE Human gene 14 encoded secreted protein fragment HHFUC40, SEQ ID NO: 123.  
 XX  
 KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;  
 KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;  
 KW inflammation; neurological disorder; Alzheimer's disease; food additive;  
 KW angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;  
 KW pregnancy-related disorder; endocrine disorder; infection; wound healing;  
 KW cell culture; chemotaxis; vulnerary; binding partner identification;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200132675-A1.  
 XX  
 PD 10-MAY-2001.  
 XX  
 PF 25-OCT-2000; 2000WO-US29363.  
 XX  
 PR 29-OCT-1999; 99US-0162239.  
 PR 30-JUN-2000; 2000US-0215139.  
 XX

PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE;  
XX  
DR WPI; 2001-328772/34.  
DR N-PSDB; AAD07822.  
XX  
PT Thirty two human secreted proteins, useful for treating cancers,  
PT hyperproliferative disorders, inflammatory disorders, neurological  
PT disorders, autoimmune diseases and cardiovascular disorders -  
XX  
PS Claim 11; Page 482; 576pp; English.  
XX  
CC AAD07809-AAD07907 represent cDNAs corresponding to 32 human secreted  
CC protein genes, and AAE03427-AAE03523 represent the proteins they encode.  
CC AAE03524-AAE03537 represent human secreted protein fragments or variants.  
CC The secreted proteins and their genes are useful for preventing, treating  
CC or ameliorating medical conditions, e.g., by protein or gene therapy.  
CC Pathological conditions can be diagnosed by determining the amount of the  
CC new protein in a sample or by determining the presence of mutations in  
CC the new genes. Specific uses are described for each of the 32 genes,  
CC based on the tissues in which they are most highly expressed, and include  
CC developing products for the diagnosis or treatment of proliferative  
CC disorders, cancer, tumours, foetal and developmental abnormalities,  
CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,  
CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,  
CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,  
CC pregnancy-related disorders, endocrine disorders, and infections. The  
CC proteins can also be used to aid wound healing and epithelial cell  
CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
CC before transplantation, for supporting cell culture of primary tissues,  
CC to regenerate tissues, to identify their cognate ligands or binding  
CC partners, and in chemotaxis, and can be used as a food additive or  
CC preservative to modify storage properties. Antibodies specific for a  
CC protein of the invention can be used in alleviating symptoms associated  
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,  
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).  
CC The present sequence represents a human secreted protein fragment of  
CC the invention.  
XX  
SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 7  
AAE03489  
ID AAE03489 standard; peptide; 5 AA.

XX  
 AC AAE03489;  
 XX  
 DT 10-AUG-2001 (first entry)  
 XX  
 DE Human gene 14 encoded secreted protein HHFUC40 fragment, SEQ ID NO:172.  
 XX  
 KW Human; secreted protein; proliferative disorder; cancer; tumour; asthma;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; skin disorder;  
 KW psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder;  
 KW inflammation; neurological disorder; Alzheimer's disease; food additive;  
 KW angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy;  
 KW pregnancy-related disorder; endocrine disorder; infection; wound healing;  
 KW cell culture; chemotaxis; vulnerary; binding partner identification;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200132675-A1.  
 XX  
 PD 10-MAY-2001.  
 XX  
 PF 25-OCT-2000; 2000WO-US29363.  
 XX  
 PR 29-OCT-1999; 99US-0162239.  
 PR 30-JUN-2000; 2000US-0215139.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Komatsoulis GA, Wei P, Baker KP, Young PE;  
 XX  
 DR WPI; 2001-328772/34.  
 DR N-PSDB; AAD07871.  
 XX  
 PT Thirty two human secreted proteins, useful for treating cancers,  
 PT hyperproliferative disorders, inflammatory disorders, neurological  
 PT disorders, autoimmune diseases and cardiovascular disorders -  
 XX  
 PS Claim 11; Page 508; 576pp; English.  
 XX  
 CC AAD07809-AAD07907 represent cDNAs corresponding to 32 human secreted  
 CC protein genes, and AAE03427-AAE03523 represent the proteins they encode.  
 CC AAE03524-AAE03537 represent human secreted protein fragments or variants.  
 CC The secreted proteins and their genes are useful for preventing, treating  
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.  
 CC Pathological conditions can be diagnosed by determining the amount of the  
 CC new protein in a sample or by determining the presence of mutations in  
 CC the new genes. Specific uses are described for each of the 32 genes,  
 CC based on the tissues in which they are most highly expressed, and include  
 CC developing products for the diagnosis or treatment of proliferative  
 CC disorders, cancer, tumours, foetal and developmental abnormalities,  
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,  
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,

CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
CC angiogenic disorders, kidney disorders, gastrointestinal disorders,  
CC pregnancy-related disorders, endocrine disorders, and infections. The  
CC proteins can also be used to aid wound healing and epithelial cell  
CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
CC before transplantation, for supporting cell culture of primary tissues,  
CC to regenerate tissues, to identify their cognate ligands or binding  
CC partners, and in chemotaxis, and can be used as a food additive or  
CC preservative to modify storage properties. Antibodies specific for a  
CC protein of the invention can be used in alleviating symptoms associated  
CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,  
CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA).  
CC The present sequence represents a human secreted protein fragment of  
CC the invention.

XX

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 2 SRL 4

#### RESULT 8

AAB49812

ID AAB49812 standard; Peptide; 5 AA.

XX

AC AAB49812;

XX

DT 02-MAR-2001 (first entry)

XX

DE Human endostatin peptide fragment SEQ ID NO: 25.

XX

KW Endostatin; antiangiogenic; angiogenesis; human; mouse; chicken;

KW cancer; inflammation; angiogenesis-dependent disease.

XX

OS Homo sapiens.

XX

PN WO200067771-A1.

XX

PD 16-NOV-2000.

XX

PF 02-MAY-2000; 2000WO-US12063.

XX

PR 06-MAY-1999; 99US-0132907.

PR 14-JUL-1999; 99US-0353333.

XX

PA (BURN-) BURNHAM INST.

XX

PI Vuori K;

XX

DR WPI; 2001-040937/05.

XX

PT Endostatin peptide comprising at least four endostatin amino acid



PT residues are e.g. angiogenesis inhibitors for treating cancer and  
PT diabetic retinopathy -  
XX  
PS Disclosure; Page 126; 146pp; English.  
XX  
CC The present invention provides endostatin peptides which can be used in  
CC the modulation of angiogenesis. This is useful in the treatment of  
CC cancers, inflammation, rheumatoid arthritis, chronic articular  
CC rheumatism, psoriasis, disorders associated with inopportune invasion of  
CC vessels such as diabetic retinopathy, neovascular glaucoma, retinopathy  
CC of prematurity, macular degeneration, corneal graft rejection,  
CC retrolental fibroplasia, rubeosis, capillary proliferation in  
CC atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent  
CC diseases include Osler-Webber syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophiliac joints and wound  
CC granulation. In addition, the peptides can be used as birth control  
CC agents.  
XX  
SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 1 SRL 3

# RESULT 9

AAE28216

ID AAE28216 standard; peptide; 5 AA.

XX

AC AAE28216;

XX

DT 27-DEC-2002 (first entry)

XX

DE Tobacco mosaic virus rGAL-25 vector peptide.

XX

KW Alpha-galactosidase; lysosomal enzyme; lysosomal storage disease;

KW therapeutic; rGAL-25.

XX

OS Tobacco mosaic virus.

XX

PN US2002088024-A1.

XX

PD 04-JUL-2002.

XX

PF 13-NOV-2001; 2001US-0993059.

XX

PR 26-JUL-2000; 2000US-0626127.

XX

PA (GARG/) GARGER S J.

PA (TURP/) TURPEN T H.

PA (KUMA/) KUMAGAI M H.

XX

PI Garger SJ, Turpen TH, Kumagai MH;

XX  
 DR WPI; 2002-681656/73.  
 XX  
 PT Novel human alpha-galactosidase polypeptide useful for treating  
 PT lysosomal storage diseases -  
 XX  
 PS Claim 1; Page 59; 88pp; English.  
 XX  
 CC The invention relates to human alpha-galactosidase truncated at the  
 CC carboxy terminus and the production of enzymatically active recombinant  
 CC human and animal lysosomal enzymes. The invention is useful for producing  
 CC lysosomal enzymes for treating lysosomal storage diseases, producing  
 CC altered or mutated proteins, enzymatically active or otherwise, to serve  
 CC as precursors or substrates for further in vivo or in vitro processing  
 CC to a specialised industrial form for research or therapeutic uses, to  
 CC produce more effective therapeutic enzyme, for producing antibodies  
 CC against lysosomal enzymes for medical diagnostic use, and in any  
 CC commercial process that involves substrate hydrolysis. The present  
 CC sequence is Tobacco mosaic virus rGAL-25 vector peptide.  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 2 SRL 4

# RESULT 10

ABG63387

ID ABG63387 standard; Protein; 5 AA.

XX

AC ABG63387;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human albumin fusion protein #62.

XX

KW Albumin fusion protein; therapeutic protein X; human albumin; HA;

KW human serum albumin; HSA; cancer; reproductive disorder;

KW digestive disorder; immune disorder; endocrine disorder;

KW haematopoietic disorder; neural disorder; connective disorder;

KW cytostatic; antiinfertility; antiinflammatory; antiulcer;

KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;

KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;

KW osteopathic; antiarthritic.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200177137-A1.

XX

PD 18-OCT-2001.

XX

PF 12-APR-2001; 2001WO-US11988.  
 XX  
 PR 12-APR-2000; 2000US-229358P.  
 PR 25-APR-2000; 2000US-199384P.  
 PR 21-DEC-2000; 2000US-256931P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Haseltine WA;  
 XX  
 DR WPI; 2002-010886/01.  
 XX  
 PT New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein -  
 XX  
 PS Claim 1; Page 628; 2102pp; English.  
 XX  
 CC The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA, also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or  
 CC disorder that may be modulated by therapeutic protein X. The albumin  
 CC extends the shelf-life of protein X, and may increase its biological  
 CC in vitro/in vivo activity. The protein is useful for treating and  
 CC diagnosing disorders such as cancer, reproductive disorders, digestive  
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders  
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders  
 CC (e.g. diabetes), haematopoietic disorders, neural disorders  
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,  
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders  
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin  
 CC fusion proteins of the invention.  
 XX  
 SQ Sequence 5 AA;  
  
 Query Match 60.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 2 SRL 4

# RESULT 11

ABG63388

ID ABG63388 standard; Protein; 5 AA.

XX

AC ABG63388;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human albumin fusion protein #63.

XX

KW Albumin fusion protein; therapeutic protein X; human albumin; HA;

KW human serum albumin; HSA; cancer; reproductive disorder;

KW digestive disorder; immune disorder; endocrine disorder;

KW haematopoietic disorder; neural disorder; connective disorder;

KW cytostatic; antiinfertility; antiinflammatory; antiulcer;  
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;  
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antiarthritic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200177137-A1.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 12-APR-2001; 2001WO-US11988.  
 XX  
 PR 12-APR-2000; 2000US-229358P.  
 PR 25-APR-2000; 2000US-199384P.  
 PR 21-DEC-2000; 2000US-256931P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Haseltine WA;  
 XX  
 DR WPI; 2002-010886/01.  
 XX  
 PT New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein -  
 XX  
 PS Claim 1; Page 628; 2102pp; English.  
 XX  
 CC The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA, also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or  
 CC disorder that may be modulated by therapeutic protein X. The albumin  
 CC extends the shelf-life of protein X, and may increase its biological  
 CC in vitro/in vivo activity. The protein is useful for treating and  
 CC diagnosing disorders such as cancer, reproductive disorders, digestive  
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders  
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders  
 CC (e.g. diabetes), haematopoietic disorders, neural disorders  
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,  
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders  
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin  
 CC fusion proteins of the invention.  
 XX  
 SQ Sequence 5 AA;  
  
 Query Match 60.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 SRL 4  
 |||  
 Db 2 SRL 4

ID ABB94397 standard; Peptide; 5 AA.  
 XX  
 AC ABB94397;  
 XX  
 DT 12-JUN-2002 (first entry)  
 XX  
 DE Ubiquitin binding monobody 411 BC loop.  
 XX  
 KW Fibronectin type 3; mutant; stabilising mutation; Fn3; antibody;  
 KW binding protein.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200204523-A2.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 11-JUL-2001; 2001WO-US21855.  
 XX  
 PR 11-JUL-2000; 2000US-217474P.  
 XX  
 PA (RESE ) RESEARCH CORP TECHNOLOGIES INC.  
 PA (KOID/) KOIDE S.  
 XX  
 PI Koide S;  
 XX  
 DR WPI; 2002-171708/22.  
 XX  
 PT New fibronectin type III molecule comprising a stabilizing mutation,  
 PT useful for introducing more mutations for better functions, and in a  
 PT wider range of applications -  
 XX  
 PS Example 10; Page 139; 164pp; English.  
 XX  
 CC The present invention relates to fibronectin type III (Fn3) molecules  
 CC comprising a stabilising mutation as compared to a wild-type Fn3. Fn3 can  
 CC be used as a scaffold to engineer artificial binding proteins.  
 CC Modifications of the Fn3 scaffold that increase its stability are useful  
 CC in that they allow the introduction of more mutations for better  
 CC functions, and that these make it possible to use Fn3-based engineered  
 CC proteins in a wider range of applications. The present sequence is a  
 CC peptide described in the exemplification of the invention.  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 1 SRL 3

RESULT 13  
 ABB94451  
 ID ABB94451 standard; Peptide; 5 AA.

XX  
 AC ABB94451;  
 XX  
 DT 12-JUN-2002 (first entry)  
 XX  
 DE Ubiquitin binding fibronectin 3 mutant BC loop SEQ ID NO: 98.  
 XX  
 KW Fibronectin type 3; mutant; stabilising mutation; Fn3; antibody;  
 KW binding protein.  
 XX  
 OS Unidentified.  
 OS Synthetic.  
 XX  
 PN WO200204523-A2.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 11-JUL-2001; 2001WO-US21855.  
 XX  
 PR 11-JUL-2000; 2000US-217474P.  
 XX  
 PA (RESE ) RESEARCH CORP TECHNOLOGIES INC.  
 PA (KOID/) KOIDE S.  
 XX  
 PI Koide S;  
 XX  
 DR WPI; 2002-171708/22.  
 XX  
 PT New fibronectin type III molecule comprising a stabilizing mutation,  
 PT useful for introducing more mutations for better functions, and in a  
 PT wider range of applications -  
 XX  
 PS Example 16; Page 156; 164pp; English.  
 XX  
 CC The present invention relates to fibronectin type III (Fn3) molecules  
 CC comprising a stabilising mutation as compared to a wild-type Fn3. Fn3 can  
 CC be used as a scaffold to engineer artificial binding proteins.  
 CC Modifications of the Fn3 scaffold that increase its stability are useful  
 CC in that they allow the introduction of more mutations for better  
 CC functions, and that these make it possible to use Fn3-based engineered  
 CC proteins in a wider range of applications. The present sequence is a  
 CC peptide described in the exemplification of the invention.  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 1 SRL 3

RESULT 14  
 AAE19260  
 ID AAE19260 standard; peptide; 5 AA.

XX  
 AC AAE19260;  
 XX  
 DT 21-MAY-2002 (first entry)  
 XX  
 DE Human recombinant alpha-galactosidase A modified peptide, rGal-25.  
 XX  
 KW Glucocerebrosidase; alpha-galactosidase; Tay-Sachs disease; plant;  
 KW enzyme replacement therapy; Niemann-Pick disease; Gaucher disease;  
 KW Fabry disease; lysosomal storage disease; human.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200208404-A2.  
 XX  
 PD 31-JAN-2002.  
 XX  
 PF 26-JUL-2001; 2001WO-US24111.  
 XX  
 PR 26-JUL-2000; 2000US-0626127.  
 XX  
 PA (LARG-) LARGE SCALE BIOLOGY CORP.  
 XX  
 PI Garger SJ, Turpen TH, Kumagai MH;  
 XX  
 DR WPI; 2002-195873/25.  
 XX  
 PT New glucocerebrosidase and alpha-galactosidase having a  
 PT post-translational modification, useful in enzyme replacement therapy  
 PT for treating lysosomal storage diseases, e.g. Gaucher disease,  
 PT Niemann-Pick disease, Fabry disease -  
 XX  
 PS Example 11; Fig 5; 102pp; English.  
 XX  
 CC The invention relates to production of lysosomal enzymes in plants  
 CC by transient expression. The invention particularly relates to  
 CC glucocerebrosidase and alpha-galactosidase having a post-translational  
 CC modification. The enzymes are useful in enzyme replacement therapy for  
 CC treating lysosomal storage diseases (e.g. Gaucher disease, Niemann-Pick  
 CC disease, Fabry disease and Tay-Sachs disease), in researches for  
 CC developing new approaches to medical treatment of lysosomal storage  
 CC diseases and in industrial processes involving enzymatic substrate  
 CC hydrolysis. The present sequence is human recombinant alpha-  
 CC galactosidase-A C-terminal modified peptide.  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 2 SRL 4

RESULT 15  
 ABP55341  
 ID ABP55341 standard; Peptide; 5 AA.  
 XX  
 AC ABP55341;  
 XX  
 DT 29-JAN-2003 (first entry)  
 XX  
 DE Cucurbita sp. peptide ELSRL SEQ ID NO:18.  
 XX  
 KW Aeromonas caviae; phaC; fusion gene; copolyester; fatty acid;  
 KW peroxisomal targeting signal sequence; peroxisome; thermoplastic;  
 KW genetically-modified plant; elastic; rubbery; multi-branched plastic;  
 KW biodegradable plastic; polyester; thermoplasticity; intrinsic elasticity;  
 KW biodegradability.  
 XX  
 OS Cucurbita sp.  
 XX  
 PN WO200272837-A1.  
 XX  
 PD 19-SEP-2002.  
 XX  
 PF 14-MAR-2002; 2002WO-JP02424.  
 XX  
 PR 14-MAR-2001; 2001JP-0072963.  
 XX  
 PA (RIKE ) RIKEN KK.  
 XX  
 PI Nakashita H, Yamaguchi I, Doi Y, Suzuki Y, Kobayashi Y, Shimizu T;  
 XX  
 DR WPI; 2003-046739/04.  
 XX  
 PT Fusion gene-transferred plants synthesizing copolymers from short-chain  
 PT fatty acid-derived monomers, applicable in producing thermoplastic,  
 PT elastic, rubbery, multi-branched and biodegradable plastics -  
 XX  
 PS Disclosure; Page 9; 56pp; Japanese.  
 XX  
 CC The present invention describes a fusion gene which is made by ligating a  
 CC gene encoding an enzyme for the synthesis of a copolyester from a monomer  
 CC derived from a 4-7C fatty acid with a gene encoding a peroxisomal  
 CC targeting signal sequence. Also described: (i) recombinant vector  
 CC containing any of the fusion genes; (ii) transformant containing the  
 CC recombinant vector; (iii) transformant plant which is obtained by  
 CC transferring the fusion gene and can express such fusion gene to give a  
 CC copolyester-synthesizing enzyme localized at the peroxisome; and  
 CC (iv) producing the polyester by culturing the transformant before  
 CC collecting such polyester from the culture medium or cultivated  
 CC material. The genetically-modified plants are applicable in producing  
 CC thermoplastic, elastic, rubbery, multi-branched and biodegradable  
 CC plastics. These transformant plants can produce polyesters with  
 CC thermoplasticity, intrinsic elasticity and biodegradability cheaply in  
 CC large quantities, without requiring petroleum resources. The present  
 CC sequence represents a peptide given in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 5 AA;



Query Match 60.0%; Score 3; DB 24; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 16

AA116474

ID AA116474 standard; peptide; 6 AA.

XX

AC AA116474;

XX

DT 06-AUG-1999 (first entry)

XX

DE Cyclic thrombin receptor peptide analogue.

XX

KW Peptide analogue; N-terminal domain; cancer; angiogenesis; metastasis;  
KW human G protein linked thrombin receptor; cyclic; antagonist; agonist;  
KW cardiovascular disease; inflammatory disease; gastrointestinal disease;  
KW osteoporosis; tissue injury; tissue repair; nerve regeneration;  
KW thrombin-mimetic study; platelet function; myocardial infarction;  
KW arterial plaque formation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 6

FT /label= Acp

FT /note= "6-amino caprionic acid"

XX

PN US5516889-A.

XX

PD 14-MAY-1996.

XX

PF 17-MAR-1995; 95US-0405933.

XX

PR 21-JUN-1993; 93US-0080643.

PR 17-MAR-1995; 95US-0405933.

XX

PA (UYTE-) UNIV TECHNOLOGIES INT INC.

XX

PI Hollenberg MD, Matsoukas JM, Moore GJ;

XX

DR WPI; 1996-251084/25.

XX

PT New cyclic peptide(s) derived from the protein G linked thrombin  
PT receptor - are agonists or antagonists for treating diseases  
PT involving this receptor, e.g. myocardial infarction

XX

PS Disclosure; Column 35; 36pp; English.

XX

CC AA116465-98 represent peptide analogues of the N-terminal domain of  
CC the human G protein linked thrombin receptor sequence. The peptides,

CC which may be cyclic, have the formula X1-Psi-X2-X3-Omega-X4 in which  
 CC Psi = any (non-)natural aromatic amino acid (aa); Omega = any  
 CC (non-)natural basic aa or derivatives; X1 is absent or is a natural  
 CC aa, 1-3C acyl or 1-5C alkyl; X2 = any natural aa; X3 is absent or is  
 CC any natural aa; and X4 is absent or is any natural aa. The peptides  
 CC are are antagonists and agonists for treating disorders involving  
 CC thrombin receptors, e.g. cardiovascular, inflammatory or  
 CC gastrointestinal diseases; osteoporosis; tissue injury and repair  
 CC (including nerve regeneration); and cancer (by inhibiting angiogenesis  
 CC and metastasis). They may also be used diagnostically and in  
 CC thrombin-mimetic studies. The peptide analogues are particularly used to  
 CC modulate platelet function (acting synergistically with aspirin-type  
 CC compounds) and so are useful in cases of myocardial infarction, as well  
 CC as to coat prostheses and to reduce arterial plaque formation.

XX

SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 17; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 1 SRL 3

# RESULT 17

AAW26814

ID AAW26814 standard; peptide; 6 AA.

XX

AC AAW26814;

XX

DT 04-NOV-1997 (first entry)

XX

DE Hexapeptide epitope sequence 10 from hepatitis C virus C33 antigen.

XX

KW HCV; infection; diagnosis; anti-C33 antibody; immunoassay;

KW competitive assay; vaccine; non-A, non-B hepatitis;

KW non structural protein; NS3.

XX

OS Hepatitis C virus.

XX

PN EP755943-A1.

XX

PD 29-JAN-1997.

XX

PF 25-JUL-1996; 96EP-0401661.

XX

PR 25-JUL-1995; 95FR-0009005.

XX

PA (INMR ) BIO MERIEUX.

XX

PI Jolivet-Reynaud C;

XX

DR WPI; 1997-101805/10.

XX

PT Polypeptide reacting with antibodies against C33 antigen of

PT hepatitis C virus - useful for diagnosis and in vaccines, also  
PT related nucleic acid, vectors and transformed cells  
XX  
PS Claim 2; Page 13; 29pp; French.  
XX  
CC The present sequence is that of a preferred polypeptide that reacts  
CC specifically with antibody against the C33 antigen of the hepatitis  
CC C virus (HCV) NS3 protein. The polypeptides have at least 5 amino  
CC acids and comprise all or part of the sequence:  
CC Asp-Gly-Ala-Lys-Phe-Ser-Ser-Arg-Leu-Gly-Ala-Ala-Gly-Ala, or  
CC a sequence derived from it. The synthetic polypeptides can be used  
CC as replacements for the native antigen, e.g. to detect HCV  
CC infection and as the active component in vaccines. They are also  
CC useful to detect, separate, purify and/or quantify anti-C33 antibody  
CC or the C33 antigen.  
XX  
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 18; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 4 SRL 6

# RESULT 18

AAY20645

ID AAY20645 standard; Protein; 6 AA.

XX

AC AAY20645;

XX

DT 22-JUL-1999 (first entry)

XX

DE Human neurofilament-L wild type protein fragment 35.

XX

KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;  
KW frameshift mutation; age-related disease; neurodegenerative disorder;  
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;  
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;  
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;  
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;  
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;  
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;  
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;  
KW high mobility group protein-C; neuroendocrine specific protein A.

XX

OS Homo sapiens.

XX

PN WO9845322-A2.

XX

PD 15-OCT-1998.

XX

PF 02-APR-1998; 98WO-IB00705.

XX

PR 10-APR-1997; 97US-0043163.

XX  
PA (UYUT-) RIJKSUNIV UTRECHT.  
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.  
PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
XX  
PI Burbach JPH, Grosveld FG, Van Leeuwen FW;  
XX  
DR WPI; 1998-609901/51.  
DR N-PSDB; AAX75758.  
XX  
PT Diagnosing disease by detecting frameshift mutations in RNA or  
PT corresponding protein mutations - used to diagnose cancer and  
PT neurological diseases, particularly Alzheimer's disease, and also  
PT for treatment and prevention with specific ribozymes or wild-type  
PT RNA  
XX  
PS Disclosure; Figure 7; 258pp; English.  
XX  
CC This invention describes a novel method for the diagnosis of a disease  
CC caused by, or associated with, an RNA molecule that has a frameshift  
CC mutation. The method is used to diagnose age-related diseases, especially  
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's  
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,  
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II  
CC and many others listed) or susceptibility to these disorders. The method  
CC allows a definitive diagnosis of Alzheimer's disease in living patients,  
CC at an early stage. It is based on the observation that disease may be  
CC caused by mutations in RNA rather than DNA. The invention describes the  
CC used of neuronal system RNA molecules, specifically proteins including  
CC beta-amyloid precursor protein (beta-APP), the microtubule associated  
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule  
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,  
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic  
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma  
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group  
CC protein-C (HMGP-C) and neuroendocrine specific protein A.  
XX  
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 19  
AAW75318  
ID AAW75318 standard; peptide; 6 AA.  
XX  
AC AAW75318;  
XX  
DT 25-MAR-2003 (updated)  
DT 02-FEB-1999 (first entry)  
XX

DE Hexapeptide #11 binds immobilised anti-Ad5 fibre head MAb 1D6.3.  
 XX  
 KW Cellular receptor; virus; immobilisation; monoclonal antibody; fibre;  
 KW viral surface protein; hexapeptide expression library; adenovirus;  
 KW major histocompatibility complex; MHC; fibronectin; gene therapy;  
 KW genetic disease; acquired immune deficiency syndrome; AIDS; cancer.  
 XX  
 OS Synthetic.  
 XX  
 PN FR2758885-A1.  
 XX  
 PD 31-JUL-1998.  
 XX  
 PF 10-JUL-1997; 97FR-0008796.  
 XX  
 PR 30-JAN-1997; 97FR-0001005.  
 PR 10-JUL-1997; 97FR-0008796.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Boulanger P, Hong SS, Karayan L;  
 XX  
 DR WPI; 1998-416493/36.  
 XX  
 PT Selection and identification of cellular receptors for viruses -  
 PT used to control attachment and entry of adenovirus into cells, e.g.  
 PT for treating infection or in gene therapy  
 XX  
 PS Example 3; Fig 2(c); 43pp; French.  
 XX  
 CC The invention relates to methods for selecting and identifying a  
 CC cellular receptor for a virus, by immobilising, on a support, a  
 CC monoclonal antibody targeted to a viral surface protein that determines  
 CC attachment of the virus to the receptor. The immobilised antibody is  
 CC incubated with a hexapeptide expression library and peptides bound to the  
 CC immobilised antibody are eluted by competitive binding with recombinant  
 CC fragments of the viral surface protein. In a reverse method, the viral  
 CC surface protein is immobilised and incubated with the peptide library. In  
 CC this case, the bound peptides are eluted by competitive binding with the  
 CC monoclonal antibody. The hexapeptides AAW75308-W75322 represent  
 CC peptides isolated by biopanning the library with an immobilised  
 CC adenovirus type 5 fibre head protein and eluted using a monoclonal  
 CC antibody (MAb) 1D6.3. The methods are used to identify peptides from MHC  
 CC Class I and/or type III fibronectin proteins that allow or facilitate  
 CC attachment by adenovirus (Ad) to host cells and/or entry into the cells,  
 CC and to identify ligands that modulate Ad infection mediated by these  
 CC peptides, e.g. to treat or prevent Ad infections or to facilitate  
 CC infection by Ad gene therapy vectors used to treat genetic diseases,  
 CC acquired immune deficiency syndrome or cancer.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	SRL	4
Db	1	SRL	3

# RESULT 20

AAW75386

ID AAW75386 standard; peptide; 6 AA.

XX

AC AAW75386;

XX

DT 02-FEB-1999 (first entry)

XX

DE Hexapeptide #11 binds immobilised anti-Ad5 fibre head MAb 1D6.3.

XX

KW Cellular receptor; virus; immobilisation; monoclonal antibody; fibre;

KW viral surface protein; hexapeptide expression library; adenovirus;

KW major histocompatibility complex; MHC; fibronectin; gene therapy;

KW genetic disease; acquired immune deficiency syndrome; AIDS; cancer.

XX

OS Synthetic.

XX

PN FR2758821-A1.

XX

PD 31-JUL-1998.

XX

PF 30-JAN-1997; 97FR-0001005.

XX

PR 30-JAN-1997; 97FR-0001005.

PR 09-SEP-1997; 97FR-0011166.

XX

PA (CNRS ) CNRS CENT NAT RECH SCI.

XX

PI Boulanger P, Hong SS, Karayan L;

XX

DR WPI; 1998-416458/36.

XX

PT Use of peptide(s) for facilitating or modulating attachment of

PT adenovirus to cells - useful for, e.g. treating or preventing

PT infection and improving uptake of gene therapy vectors

XX

PS Example 3; Fig 2(c); 48pp; French.

XX

CC The invention relates to methods for selecting and identifying a  
 CC cellular receptor for a virus, by immobilising, on a support, a  
 CC monoclonal antibody targeted to a viral surface protein that determines  
 CC attachment of the virus to the receptor. The immobilised antibody is  
 CC incubated with a hexapeptide expression library and peptides bound to the  
 CC immobilised antibody are eluted by competitive binding with recombinant  
 CC fragments of the viral surface protein. In a reverse method, the viral  
 CC surface protein is immobilised and incubated with the peptide library. In  
 CC this case, the bound peptides are eluted by competitive binding with the  
 CC monoclonal antibody. The hexapeptides AAW75376-W75390 represent  
 CC peptides isolated by biopanning the library with an immobilised  
 CC adenovirus type 5 fibre head protein and eluted using a monoclonal  
 CC antibody (MAb) 1D6.3. The methods are used to identify peptides from MHC  
 CC Class I and/or type III fibronectin proteins that allow or facilitate

CC attachment by adenovirus (Ad) to host cells and/or entry into the cells,  
CC and to identify ligands that modulate Ad infection mediated by these  
CC peptides, e.g. to treat or prevent Ad infections or to facilitate  
CC infection by Ad gene therapy vectors used to treat genetic diseases,  
CC acquired immune deficiency syndrome or cancer.

XX

SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 19; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 1 SRL 3

#### RESULT 21

AA55284

ID AA55284 standard; peptide; 6 AA.

XX

AC AA55284;

XX

DT 07-JAN-2000 (first entry)

XX

DE ATCC HB 11885 monoclonal antibody 9079 releasing peptide SEQ ID NO:178.

XX

KW Antibody releasing peptide; CD34; hybridoma; binding; antigen;  
KW cell surface antigen; identification; haematopoietic stem cell;  
KW tumour; cancer; immune system; therapy; displacement.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN US5968753-A.

XX

PD 19-OCT-1999.

XX

PF 07-JUN-1995; 95US-0482228.

XX

PR 14-JUN-1994; 94US-0259427.

XX

PA (NEXE-) NEXELL THERAPEUTICS INC.

XX

PI Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;

PI Al-Abdaly FA;

XX

DR WPI; 1999-590399/50.

XX

PT Short peptides useful for displacing antibodies from cell surface  
PT antigens. -

XX

PS Example 9; Column 33; 81pp; English.

XX

CC The present invention describes peptides of 4-17 amino acids which  
CC displace either the anti-CD34 monoclonal antibody designated 561, the  
CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC

CC HB-11646 (designated 9069), the anti-CD34 antibody produced by  
CC hybridoma ATCC HB-11885 (9079), or the anti-human breast cancer  
CC antibody produced by hybridoma ATCC HB-11884 (9187), from a cell  
CC surface antigen on a target cell. The peptides are useful for  
CC displacing antibodies bound to cell surfaces to release cells that  
CC have been positively selected by antibody-mediated binding to beads  
CC or other solid support. AAY55107 to AAY55319 represent peptides used in  
CC the exemplification of the present invention.

XX

SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 2 SRL 4

## RESULT 22

AAY87030

ID AAY87030 standard; Peptide; 6 AA.

XX

AC AAY87030;

XX

DT 09-MAY-2000 (first entry)

XX

DE Human haematopoietic CD34+ cell binding peptide SEQ ID #178.

XX

KW Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody;

KW non-enzymatic cell selection method; haematopoietic stem cell;

KW haematopoietic progenitor cell; antibody 561; breast cancer cell;

KW antibody 9187; cell surface determinant; diagnostic cell based assay.

XX

OS Homo sapiens.

XX

PN US6017719-A.

XX

PD 25-JAN-2000.

XX

PF 07-JUN-1995; 95US-0482528.

XX

PR 14-JUN-1994; 94US-0259427.

XX

PA (NEXE-) NEXELL THERAPEUTICS INC.

XX

PI Guillermo R, Helgersen SL, Deans RJ, Tseng-Law J, Kobori JA;

PI Al-Abdaly FA;

XX

DR WPI; 2000-136676/12.

XX

PT Non-enzymatic method for the positive selection of target cells from a

PT heterogeneous cell suspension, useful for selecting human breast cancer

PT cells from a patient's blood or bone marrow -

XX

PS Example 9; Column 37; 82pp; English.



XX  
 CC This sequence represents a human haematopoietic CD34+ cell binding  
 CC peptide, and was used to test the method of the invention. The method is  
 CC a non-enzymatic method for the positive selection of one or more target  
 CC cells from a heterogeneous cell suspension, by using specific peptides  
 CC which effect the displacement and release of a specific target cell  
 CC from a specific monoclonal antibody. The method is useful for positive  
 CC selection and specific release of target human haematopoietic  
 CC stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and  
 CC the antibody 561. The method is also useful for positive selection and  
 CC specific release of target human breast cancer cells, bound by the  
 CC monoclonal anti-breast cancer antibody 9187, from a patient's blood or  
 CC bone marrow. Identification of peptide epitopes for antibodies which  
 CC recognise cell surface determinants also allows construction of  
 CC diagnostic cell based assays. The peptide mediated release is enzyme free  
 CC and thus leaves the cell surface proteins intact. Moreover, peptide  
 CC mediated release leaves the target cell free of bound antibody or  
 CC antibody fragments. The method also produces a high yield of functional  
 CC target cells and is relatively inexpensive to carry out.  
 XX  
 SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 21; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 2 SRL 4

# RESULT 23

AAY43709

ID AAY43709 standard; peptide; 6 AA.

XX

AC AAY43709;

XX

DT 11-FEB-2000 (first entry)

XX

DE Sequence of the second loop of an omega conotoxin.

XX

KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;  
 KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;  
 KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;  
 KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX

OS Synthetic.

OS Conus catus.

XX

PN WO9954350-A1.

XX

PD 28-OCT-1999.

XX

PF 16-APR-1999; 99WO-AU00288.

XX

PR 16-APR-1998; 98AU-0002989.

PR 01-FEB-1999; 99AU-0008419.

XX  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;  
XX  
DR WPI; 2000-013226/01.  
XX  
PT Novel peptides used for the treatment of disorders and diseases where  
PT blockage of the N-type calcium channels is required -  
XX  
PS Claim 5; Page 45; 81pp; English.  
XX  
CC The present sequence represents the second loop of an isolated,  
CC synthetic, or recombinant omega-conotoxin. Omega-conotoxins are  
CC isolated from venoms of predatory marine snails, and have a  
CC selectivity for N-type calcium channels over P/Q type channels, and so  
CC block N-type calcium channels. The omega-conotoxins of the invention  
CC can be used in any disease or disorder where blockage of N-type calcium  
CC channels is required, e.g. in the reduction of neuronal damage following  
CC ischemia, production of analgesia, or enhancement of opiate analgesia,  
CC in the treatment of schizophrenia, stimulant induced psychoses,  
CC hypertension, inflammation, and diseases which cause bronchotension,  
CC and also in the inhibition of progression of neuropathic pain. They can  
CC also be used in a screen to identify compounds with activity at N-type  
CC voltage sensitive calcium channels.  
XX  
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 1 SRL 3

#### RESULT 24

AAY43740

ID AAY43740 standard; peptide; 6 AA.

XX

AC AAY43740;

XX

DT 11-FEB-2000 (first entry)

XX

DE Sequence of the second loop of an omega conotoxin.

XX

KW Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;  
KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;  
KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;  
KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX

OS Synthetic.

OS Conus sp.

XX

FH Key Location/Qualifiers

FT Modified-site 4

```

FT          /label= Nle
FT          /note= "norleucine"
XX
PN  WO9954350-A1.
XX
PD  28-OCT-1999.
XX
PF  16-APR-1999;   99WO-AU00288.
XX
PR  16-APR-1998;   98AU-0002989.
PR  01-FEB-1999;   99AU-0008419.
XX
PA  (UYQU ) UNIV QUEENSLAND.
XX
PI  Drinkwater RD,  Lewis RJ,  Alewood PF,  Nielsen KJ;
XX
DR  WPI; 2000-013226/01.
XX
PT  Novel peptides used for the treatment of disorders and diseases where
PT  blockage of the N-type calcium channels is required  -
XX
PS  Claim 5; Page 45; 81pp; English.
XX
CC  The present sequence represents the second loop of an isolated,
CC  synthetic, or recombinant omega-conotoxin. Omega-conotoxins are
CC  isolated from venoms of predatory marine snails, and have a
CC  selectivity for N-type calcium channels over P/Q type channels, and so
CC  block N-type calcium channels. The omega-conotoxins of the invention
CC  can be used in any disease or disorder where blockage of N-type calcium
CC  channels is required, e.g. in the reduction of neuronal damage following
CC  ischemia, production of analgesia, or enhancement of opiate analgesia,
CC  in the treatment of schizophrenia, stimulant induced psychoses,
CC  hypertension, inflammation, and diseases which cause bronchotension,
CC  and also in the inhibition of progression of neuropathic pain. They can
CC  also be used in a screen to identify compounds with activity at N-type
CC  voltage sensitive calcium channels.
XX
SQ  Sequence    6 AA;

Query Match          60.0%;  Score 3;  DB 21;  Length 6;
Best Local Similarity 100.0%;  Pred. No. 9.3e+05;
Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

QY          2 SRL 4
           |||
Db          1 SRL 3

```

RESULT 25

AAM97492

ID AAM97492 standard; Peptide; 6 AA.

XX

AC AAM97492;

XX

DT 24-JAN-2002 (first entry)

XX

DE Human peptide #767 encoded by a SNP oligonucleotide.

XX  
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;  
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
KW multifactorial disease; autoimmune disease; infection;  
KW nervous system disease.

XX  
OS Homo sapiens.

XX  
PN WO200147944-A2.

XX  
PD 05-JUL-2001.

XX  
PF 28-DEC-2000; 2000WO-US35498.

XX  
PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

XX  
PA (CURA-) CURAGEN CORP.

XX  
PI Shimkets RA, Leach M;

XX  
DR WPI; 2001-465210/50.

XX  
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
PT oncogenes and histones, useful for diagnosing and treating, e.g.  
PT cancer, autoimmune diseases and infections -

XX  
PS Disclosure; Page 3836; 4143pp; English.

XX  
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
CC encoding polymorphic variants of proteins related to amylases, amyloid  
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,  
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
CC complement related proteins, cytochromes, kinesins, cytokines,  
CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
CC The present sequence is a peptide encoded by one such oligonucleotide.  
CC The oligonucleotides and the peptides encoded by them may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate expression of the proteins listed above. Disorders that may  
CC be prevented, diagnosed and/or treated include multifactorial diseases  
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus  
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
CC system and an infection of pathogenic organisms.

XX  
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

Db                    |||  
                      3 SRL 5

RESULT 26

AAB49814

ID    AAB49814 standard; Peptide; 6 AA.

XX

AC    AAB49814;

XX

DT    02-MAR-2001    (first entry)

XX

DE    Human endostatin peptide fragment SEQ ID NO: 27.

XX

KW    Endostatin; antiangiogenic; angiogenesis; human; mouse; chicken;

KW    cancer; inflammation; angiogenesis-dependent disease.

XX

OS    Homo sapiens.

XX

PN    WO200067771-A1.

XX

PD    16-NOV-2000.

XX

PF    02-MAY-2000; 2000WO-US12063.

XX

PR    06-MAY-1999;    99US-0132907.

PR    14-JUL-1999;    99US-0353333.

XX

PA    (BURN-) BURNHAM INST.

XX

PI    Vuori K;

XX

DR    WPI; 2001-040937/05.

XX

PT    Endostatin peptide comprising at least four endostatin amino acid

PT    residues are e.g. angiogenesis inhibitors for treating cancer and

PT    diabetic retinopathy -

XX

PS    Disclosure; Page 127; 146pp; English.

XX

CC    The present invention provides endostatin peptides which can be used in  
CC    the modulation of angiogenesis. This is useful in the treatment of  
CC    cancers, inflammation, rheumatoid arthritis, chronic articular  
CC    rheumatism, psoriasis, disorders associated with inopportune invasion of  
CC    vessels such as diabetic retinopathy, neovascular glaucoma, retinopathy  
CC    of prematurity, macular degeneration, corneal graft rejection,  
CC    retrolental fibroplasia, rubeosis, capillary proliferation in  
CC    atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent  
CC    diseases include Osler-Webber syndrome, myocardial angiogenesis, plaque  
CC    neovascularisation, telangiectasia, haemophiliac joints and wound  
CC    granulation. In addition, the peptides can be used as birth control  
CC    agents.

XX

SQ    Sequence    6 AA;

Query Match                    60.0%;    Score 3;    DB 22;    Length 6;  
Best Local Similarity    100.0%;    Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 27

AAB49815

ID AAB49815 standard; Peptide; 6 AA.

XX

AC AAB49815;

XX

DT 02-MAR-2001 (first entry)

XX

DE Human endostatin peptide fragment SEQ ID NO: 28.

XX

KW Endostatin; antiangiogenic; angiogenesis; human; mouse; chicken;  
KW cancer; inflammation; angiogenesis-dependent disease.

XX

OS Homo sapiens.

XX

PN WO200067771-A1.

XX

PD 16-NOV-2000.

XX

PF 02-MAY-2000; 2000WO-US12063.

XX

PR 06-MAY-1999; 99US-0132907.

PR 14-JUL-1999; 99US-0353333.

XX

PA (BURN-) BURNHAM INST.

XX

PI Vuori K;

XX

DR WPI; 2001-040937/05.

XX

PT Endostatin peptide comprising at least four endostatin amino acid  
PT residues are e.g. angiogenesis inhibitors for treating cancer and  
PT diabetic retinopathy -

XX

PS Disclosure; Page 127; 146pp; English.

XX

CC The present invention provides endostatin peptides which can be used in  
CC the modulation of angiogenesis. This is useful in the treatment of  
CC cancers, inflammation, rheumatoid arthritis, chronic articular  
CC rheumatism, psoriasis, disorders associated with inopportune invasion of  
CC vessels such as diabetic retinopathy, neovascular glaucoma, retinopathy  
CC of prematurity, macular degeneration, corneal graft rejection,  
CC retrolental fibroplasia, rubeosis, capillary proliferation in  
CC atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent  
CC diseases include Osler-Webber syndrome, myocardial angiogenesis, plaque  
CC neovascularisation, telangiectasia, haemophiliac joints and wound  
CC granulation. In addition, the peptides can be used as birth control  
CC agents.

XX

SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 1 SRL 3

RESULT 28

ABG60376

ID ABG60376 standard; Peptide; 6 AA.

XX

AC ABG60376;

XX

DT 30-JUL-2002 (first entry)

XX

DE Selective targeting peptide #51.

XX

KW Targeting peptide; cancer; arthritis; diabetes; inflammatory disease;  
KW atherosclerosis; autoimmune disease; bacterial infection; apoptosis;  
KW viral infection; cardiovascular disease; degenerative disease; ischaemia;  
KW inflammation; macular degeneration; antiinflammatory; antidiabetic;  
KW cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;  
KW gene therapy.

XX

OS Synthetic.

XX

PN WO200220769-A1.

XX

PD 14-MAR-2002.

XX

PF 07-SEP-2001; 2001WO-US27692.

XX

PR 08-SEP-2000; 2000US-231266P.

PR 17-JAN-2001; 2001US-0765101.

XX

PA (TEXA ) UNIV TEXAS SYSTEM.

XX

PI Arap W, Pasqualini R;

XX

DR WPI; 2002-415731/44.

XX

PT Targeting peptides identified by phage display, useful for targeting  
PT delivery to an organ or tissue, particularly for treating a disease,  
PT e.g. cancer, inflammatory or autoimmune diseases, infections or  
PT cardiovascular disease -

XX

PS Claim 22; Page 65; 317pp; English.

XX

CC The invention relates to an isolated peptide of 100 amino acids or less  
CC in size useful for targeting delivery to an organ or tissue, particularly  
CC for treating a disease, e.g. cancer, arthritis, diabetes, inflammatory  
CC disease, atherosclerosis, autoimmune disease, bacterial infection, viral  
CC infection, cardiovascular disease or degenerative disease. The peptide is  
CC also useful for inducing apoptosis, particularly to a subject with

CC ischaemia, cancer, arthritis, diabetes, cardiovascular disease,  
 CC inflammation or macular degeneration. Furthermore, the peptide is useful  
 CC for diagnosing the diseases cited above. Targeting peptides of the  
 CC invention can also be used to deliver an agent to a foetus, by attaching  
 CC a peptide to the agent and administering the peptide to a pregnant  
 CC subject. Sequences ABG60326-ABG60574 represent selective targeting  
 CC peptides of the invention.

XX

SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 4 SRL 6

# RESULT 29

AAP20402

ID AAP20402 standard; Protein; 7 AA.

XX

AC AAP20402;

XX

DT 25-MAR-2003 (updated)

DT 30-NOV-1992 (first entry)

XX

DE Secretin precursor formation peptide 4.

XX

KW Strong acid; digestive canal hormone; pancreas; gastrin; pepsin;  
 KW insulin.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "But protected"

FT Modified-site 2

FT /note= "PhSO2 ring substd. by 1, 2 or 3 alkyl or  
 FT alkoxy gps."

FT Modified-site 4

FT /note= "PhSO2 ring substd. by 1, 2 or 3 alkyl or  
 FT alkoxy gps."

FT Modified-site 5

FT /note= "OBut protected"

FT Modified-site 6

FT /note= "But protected"

XX

PN EP47997-A.

XX

PD 24-MAR-1982.

XX

PF 11-SEP-1981; 81EP-0107186.

XX

PR 11-SEP-1980; 80JP-0125262.

XX



PA (EISA ) EISAI CO LTD.  
 XX  
 PI Uchiyama M, Sato T, Yoshino H, Tsuchiya Y, Konishi M;  
 PI Tsujii M, Hisatake Y, Koiwa A;  
 XX  
 DR WPI; 1982-24409E/13 (24409E).  
 XX  
 PT Heptacosa:peptide(s) - useful for high yield conversion to high  
 PT purity secretin on strong acid treatment  
 XX  
 PS Claim 10; Page 45; 47pp; English.  
 XX  
 CC The sequence in AAP20398 is a precursor for the production of  
 CC secretin. The peptide sequences given in AAP20399-402 are peptides  
 CC which are useful in the production of this precursor. The precursor is  
 CC treated with strong acid in the preparation of secretin. Secretin is  
 CC one of the digestive canal hormones and is useful in promotion of  
 CC pancreatic external secretin, controlling gastrin-stimulating secretin  
 CC of the stomach acid, releasing insulin, stimulating secretin of pepsin  
 CC and decomposing fat. It is used as a pancreatic-function examining  
 CC agent and a medicine for curing duodenal ulcers etc.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 1 SRL 3

# RESULT 30

AAP30020

ID AAP30020 standard; peptide; 7 AA.

XX

AC AAP30020;

XX

DT 25-MAR-2003 (updated)

DT 03-SEP-1992 (first entry)

XX

DE Intermediate of secretin synthesis.

XX

KW Digestive; hormone; industrial; insulin; gastrin; pancreas; duodenal;  
 KW ulcers.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /label= X-Ser-t-Bu

FT /note= "X= H or benzyloxycarbonyl"

FT Modified-site 2

FT /label= Arg-Tos

FT Modified-site 4

FT /label= Arg-Tos  
 FT Modified-site 5  
 FT /label= Asp-O-t-Bu  
 FT Modified-site 6  
 FT /label= Ser-t-Bu  
 XX  
 PN JP58152848-A.  
 XX  
 PD 10-SEP-1983.  
 XX  
 PF 05-MAR-1982; 82JP-0034029.  
 XX  
 PR 07-SEP-1981; 81JP-0140717.  
 XX  
 PA (EISA ) EISAI CO LTD.  
 XX  
 DR WPI; 1983-791972/42.  
 XX  
 PT Hepta:peptide(s) useful as intermediates to secretin - a  
 PT digestive tract hormone useful in treating duodenal ulcers  
 XX  
 PS Claim 1; Page 1; 13pp; Japanese.  
 XX  
 CC The peptide is an intermediate in the industrial synthesis of  
 CC secretin, a digestive tract hormone. Secretin has various  
 CC pharmaceutical actions such as pancreatic exocrinogenic,  
 CC gastrin stimulating, gastric acid secretion inhibitory,  
 CC insulin releasing, pepsin secretion promoting and adipolytic  
 CC action. It is used as a reagent for study of pancreatic  
 CC function or as a remedy for duodenal ulcers.  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 7 AA;  
  
 Query Match 60.0%; Score 3; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 SRL 4  
 |||  
 Db 1 SRL 3

RESULT 31  
 AAW11186  
 ID AAW11186 standard; Peptide; 7 AA.  
 XX  
 AC AAW11186;  
 XX  
 DT 15-JAN-1998 (first entry)  
 XX  
 DE Brain homing peptide.  
 XX  
 KW Brain homing peptide; in vivo panning; screening; phage display;  
 KW drug delivery.  
 XX

OS Synthetic.  
 XX  
 PN WO9710507-A1.  
 XX  
 PD 20-MAR-1997.  
 XX  
 PF 10-SEP-1996; 96WO-US14600.  
 XX  
 PR 11-SEP-1995; 95US-0526710.  
 PR 11-SEP-1995; 95US-0526708.  
 XX  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX  
 PI Pasqualini R, Ruoslahti E;  
 XX  
 DR WPI; 1997-202359/18.  
 XX  
 PT Obtaining compound that homes to selected organ or tissue - by in  
 PT vivo panning method, specifically to identify brain, kidney,  
 PT angiogenic vasculature or tumour tissue homing peptide(s)  
 XX  
 PS Disclosure; Page 45; 75pp; English.  
 XX  
 CC This synthetic peptide is an example of a brain-homing peptide  
 CC that was identified using a claimed method for obtaining  
 CC molecules that home to a selected organ or tissue. This in vivo  
 CC panning method typically involves administering a phage display  
 CC library to a subject, and identifying expressed peptides which  
 CC home to the desired organ or tissue, e.g. brain, kidney, angiogenic  
 CC vascular tissue or tumour tissue. The isolated peptides (see  
 CC AAW13412-52, AAW11181-86) can be used to target e.g. drugs, toxins or  
 CC labels to the selected organ/tissue (claimed) or to identify and/or  
 CC isolate target molecules (claimed). The peptides can be directly  
 CC identified in vivo, as compared to prior art in vitro screening  
 CC methods, which require further examination to see if they maintain  
 CC specificity in vivo.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 18; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
 |||  
 Db 3 SRL 5

# RESULT 32

AAW27419

ID AAW27419 standard; peptide; 7 AA.

XX

AC AAW27419;

XX

DT 19-DEC-1997 (first entry)

XX

DE CDR2 from light chain variable region of KM1259 antibody.

XX  
 KW Complementarity determining region; CDR; light chain; treatment;  
 KW variable region; murine; mouse; human; interleukin 5; IL-5;  
 KW receptor; alpha chain; monoclonal antibody; hybridoma; detection;  
 KW assay; diagnosis; allergic respiratory disease; chronic bronchitis;  
 XX  
 OS Mus spp.  
 XX  
 PN WO9710354-A1.  
 XX  
 PD 20-MAR-1997.  
 XX  
 PF 11-SEP-1996; 96WO-JP02588.  
 XX  
 PR 11-SEP-1995; 95JP-0232384.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Anazawa H, Furuya A, Hanai N, Iida A, Koike M;  
 PI Nakamura K, Takatsu K;  
 XX  
 DR WPI; 1997-202249/18.  
 XX  
 PT Antibody against alpha-chain of human interleukin 5 receptor -  
 PT useful for diagnosis and treatment of respiratory allergic diseases,  
 PT e.g. chronic bronchitis  
 XX  
 PS Claim 8; Page 165; 238pp; Japanese.  
 XX  
 CC The present sequence is complementarity determining region 2 (CDR2)  
 CC from the light chain variable region of the murine anti-human  
 CC interleukin 5 receptor alpha chain (hIL-5R alpha) monoclonal  
 CC antibody (MAb) KM1259. KM1259 is produced by the hybridoma  
 CC FERM BP-5134, which was prepared by immunising Balb/c mice with  
 CC hIL-5R alpha, fusing spleen cells obtained from the mice with mouse  
 CC myeloma P3-U1 cells and screening the resultant hybridomas. The MAb  
 CC can be used to detect or assay for hIL-5R alpha and cells  
 CC expressing it on their surface, especially to diagnose allergic  
 CC respiratory diseases, e.g. chronic bronchitis. It can also be used  
 CC to treat such diseases.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 18; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 3 SRL 5

RESULT 33  
 AAY48768  
 ID AAY48768 standard; Peptide; 7 AA.  
 XX  
 AC AAY48768;

XX  
 DT 20-MAR-2003 (updated)  
 DT 10-DEC-1999 (first entry)  
 XX  
 DE Membrane dipeptidase-binding gut homing peptide #13.  
 XX  
 KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;  
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;  
 KW membrane dipeptidase.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9946284-A2.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 10-MAR-1999; 99WO-US05284.  
 XX  
 PR 13-MAR-1998; 98US-0042107.  
 PR 26-FEB-1999; 99US-0258754.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Rajotte D, Pasqualini R, Ruoslahti EI;  
 XX  
 DR WPI; 1999-571717/48.  
 XX  
 PT New peptides which selectively home to organs or tissues, used for,  
 PT e.g. identifying target ligands and for therapy of pathological  
 PT conditions -  
 XX  
 PS Example 6; Page 147; 193pp; English.  
 XX  
 CC The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ  
 CC or tissue, for identifying a target molecule expressed by an organ or  
 CC tissue or for treating an organ or tissue pathology, where the organ or  
 CC tissue is selected from prostate, lung, skin, retina, pancreas, gut,  
 CC ovary, adrenal gland, liver, and lymph node. The peptide bind to the  
 CC membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences  
 CC which are used in the exemplification of the present invention.  
 CC (Updated on 20-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 1 SRL 3

RESULT 34  
 AAY48912

ID AAY48912 standard; Peptide; 7 AA.  
 XX  
 AC AAY48912;  
 XX  
 DT 20-MAR-2003 (updated)  
 DT 10-DEC-1999 (first entry)  
 XX  
 DE Membrane dipeptidase-binding prostate homing peptide #28.  
 XX  
 KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;  
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;  
 KW membrane dipeptidase.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9946284-A2.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 10-MAR-1999; 99WO-US05284.  
 XX  
 PR 13-MAR-1998; 98US-0042107.  
 PR 26-FEB-1999; 99US-0258754.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Rajotte D, Pasqualini R, Ruoslahti EI;  
 XX  
 DR WPI; 1999-571717/48.  
 XX  
 PT New peptides which selectively home to organs or tissues, used for,  
 PT e.g. identifying target ligands and for therapy of pathological  
 PT conditions -  
 XX  
 PS Example 6; Page 151; 193pp; English.  
 XX  
 CC The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ  
 CC or tissue, for identifying a target molecule expressed by an organ or  
 CC tissue or for treating an organ or tissue pathology, where the organ or  
 CC tissue is selected from prostate, lung, skin, retina, pancreas, gut,  
 CC ovary, adrenal gland, liver, and lymph node. The peptide bind to the  
 CC membrane dipeptidase (MDP). AAY48618 to AAY49066 represent sequences  
 CC which are used in the exemplification of the present invention.  
 CC (Updated on 20-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 7 AA;  
  
 Query Match 60.0%; Score 3; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 SRL 4  
 |||  
 Db 4 SRL 6

RESULT 35

AAY16941

ID AAY16941 standard; peptide; 7 AA.

XX

AC AAY16941;

XX

DT 20-JUL-1999 (first entry)

XX

DE Heat shock protein (hsp) binding peptide.

XX

KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;  
KW surface protein; tethering peptide; chaperone process; cytokine; cancer;  
KW neoplastic disease; infectious disease; bacterium; immune system; fungus;  
KW acquired immune deficiency; autoimmune disease.

XX

OS Synthetic.

XX

PN W09922761-A1.

XX

PD 14-MAY-1999.

XX

PF 22-OCT-1998; 98WO-US22335.

XX

PR 31-OCT-1997; 97US-0961707.

XX

PA (SLOK ) SLOAN KETTERING INST CANCER RES.

XX

PI Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;

PI Ouerfelli O, Rothman JE;

XX

DR WPI; 1999-313177/26.

XX

PT Identifying peptides which bind heat shock proteins

XX

PS Examples; Page 22; 155pp; English.

XX

CC The invention relates to conjugate peptides engineered to noncovalently  
CC bind to heat shock proteins (hsp). A method of identifying a hsp binding  
CC peptide comprises (a) contacting a phage display library having  
CC bacteriophage expressing, in a surface protein, inserted peptides with a  
CC hsp target, and bound to a benzoquinone ansamycin antibiotic (BAA), in a  
CC physiologic binding buffer; (b) isolating a phage binding to the hsp  
CC target; and (c) identifying the inserted peptide expressed. The peptides  
CC which bind to a hsp can be used as tethering peptides for a hsp which may  
CC serve as an accessory in a chaperone process and/or may comprise a  
CC cytokine. They can also be coupled to antigens to induce an immune  
CC response. Such compositions can be used for treating neoplastic disease,  
CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,  
CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a  
CC disease of the immune system, e.g. acquired immune deficiencies or  
CC autoimmune diseases.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 36

AAY05017

ID AAY05017 standard; peptide; 7 AA.

XX

AC AAY05017;

XX

DT 16-JUN-1999 (first entry)

XX

DE Tumour antigen antibody light chain CDR2 clone F19.

XX

KW Tumour antigen; antibody; CDR; complementarity determining region;  
KW binding molecule identification; tumour-specific binding polypeptide;  
KW cancer therapy; light chain.

XX

OS Homo sapiens.

XX

PN WO9906834-A2.

XX

PD 11-FEB-1999.

XX

PF 04-AUG-1998; 98WO-US16280.

XX

PR 04-AUG-1997; 97US-0905825.

PR 04-AUG-1997; 97US-1112222.

XX

PA (IXSY-) IXSYS INC.

XX

PI Huse WD, Watkins JD, Wu H;

XX

DR WPI; 1999-153951/13.

DR N-PSDB; AAX28194.

XX

PT Identifying binding molecules for ligands, particularly tumour  
PT antigens - by selectively immobilising a population of binding  
PT molecules to a solid support and screening for binding to two or  
PT more ligands

XX

PS Claim 15; Page 57; 80pp; English.

XX

CC This sequence represents a light chain complementarity determining  
CC region (CDR) from a tumour antigen specific antibody.

CC The invention relates to a method for identifying a binding molecule  
CC having selective affinity for a ligand comprising: (a) selectively  
CC immobilising a diverse population of binding molecules to a solid  
CC support; (b) simultaneously contacting the diverse population immobilised  
CC on the solid support with 2 or more ligands; and (c) determining at least  
CC one binding molecule which selectively binds to one or more of the  
CC ligands. The method allows for the rapid and efficient methods for the  
CC identification of binding molecules which exhibit selective affinity for  
CC one or more ligands of interest. They are used particularly for



CC identifying tumour-specific binding polypeptides which can be used as  
CC targeting agents for cancer therapy that minimises impact on non-tumour  
CC tissues.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 3 SRL 5

#### RESULT 37

AAAY05021

ID AAY05021 standard; peptide; 7 AA.

XX

AC AAY05021;

XX

DT 16-JUN-1999 (first entry)

XX

DE Tumour antigen antibody light chain CDR2 clone F26.

XX

KW Tumour antigen; antibody; CDR; complementarity determining region;  
KW binding molecule identification; tumour-specific binding polypeptide;  
KW cancer therapy; light chain.

XX

OS Homo sapiens.

XX

PN WO9906834-A2.

XX

PD 11-FEB-1999.

XX

PF 04-AUG-1998; 98WO-US16280.

XX

PR 04-AUG-1997; 97US-0905825.

PR 04-AUG-1997; 97US-1112222.

XX

PA (IXSY-) IXSYS INC.

XX

PI Huse WD, Watkins JD, Wu H;

XX

DR WPI; 1999-153951/13.

DR N-PSDB; AAX28198.

XX

PT Identifying binding molecules for ligands, particularly tumour  
PT antigens - by selectively immobilising a population of binding  
PT molecules to a solid support and screening for binding to two or  
PT more ligands

XX

PS Claim 15; Page 57; 80pp; English.

XX

CC This sequence represents a light chain complementarity determining  
CC region (CDR) from a tumour antigen specific antibody.

CC The invention relates to a method for identifying a binding molecule

CC having selective affinity for a ligand comprising: (a) selectively  
CC immobilising a diverse population of binding molecules to a solid  
CC support; (b) simultaneously contacting the diverse population immobilised  
CC on the solid support with 2 or more ligands; and (c) determining at least  
CC one binding molecule which selectively binds to one or more of the  
CC ligands. The method allows for the rapid and efficient methods for the  
CC identification of binding molecules which exhibit selective affinity for  
CC one or more ligands of interest. They are used particularly for  
CC identifying tumour-specific binding polypeptides which can be used as  
CC targeting agents for cancer therapy that minimises impact on non-tumour  
CC tissues.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 3 SRL 5

#### RESULT 38

AAB28344

ID AAB28344 standard; Peptide; 7 AA.

XX

AC AAB28344;

XX

DT 16-FEB-2001 (first entry)

XX

DE Neuropeptide NPFII.

XX

KW Pesticidal; mosquito; Trypsin Modulating Oostatic Factor;

KW TMOF; hormone; trypsin biosynthesis; digestive enzyme; neuropeptide;

KW NPFII.

XX

OS Leptinotarsa decemlineata.

XX

PN WO200063235-A2.

XX

PD 26-OCT-2000.

XX

PF 18-APR-2000; 2000WO-US10375.

XX

PR 21-APR-1999; 99US-0296113.

XX

PA (UYFL ) UNIV FLORIDA RES FOUND INC.

XX

PI Borovsky D;

XX

DR WPI; 2000-687157/67.

XX

PT Recombinant plant cell transformed to express a polynucleotide encoding

PT a pesticidal agent such as trypsin modulating oostatic factor compounds

PT or neuropeptide F compounds, is useful for controlling plant pests -

XX

PS Claim 20; Page 9; 48pp; English.

XX

CC The present sequence is neuropeptide NPFII from Colorado potato beetle.  
CC This sequence was used to produce a recombinant plant cell. The  
CC recombinant plant cell is useful for controlling agricultural pests, in  
CC particular insects, and is also useful for inhibiting the production of  
CC digestive enzymes in a pest to control the pest. The recombinant plant  
CC cell may also comprise mosquito Trypsin Modulating Oostatic Factor  
CC (TMOF) (AAB28346). TMOF is a hormone, which regulates the biosynthesis of  
CC the digestive enzyme trypsin. TMOF is synthesised in the follicular  
CC epithelium of the ovary 2-30 hours after a blood meal and is released  
CC into the haemolymph, binding to the TMOF receptor on the midgut  
CC epithelial cells, signalling the termination of trypsin biosynthesis.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 3 SRL 5

#### RESULT 39

AAB36149

ID AAB36149 standard; peptide; 7 AA.

XX

AC AAB36149;

XX

DT 20-FEB-2001 (first entry)

XX

DE Neuropeptide NPFII.

XX

KW Pesticidal; trypsin biosynthesis; neuropeptide F; NPF;

KW trypsin modulating oostatic factor; TMOF; NPFI.

XX

OS Synthetic.

XX

PN WO200062620-A2.

XX

PD 26-OCT-2000.

XX

PF 18-APR-2000; 2000WO-US10247.

XX

PR 21-APR-1999; 99US-0295846.

XX

PA (UYFL ) UNIV FLORIDA RES FOUND INC.

XX

PI Borovsky D, Schlesinger Y, Nauwelaers SMI;

XX

DR WPI; 2000-672705/65.

XX

PT Novel recombinant host useful for controlling pest such as mosquitoes,

PT flesh flies, fleas, sand flies, house flies and dog flies comprises

PT polynucleotide encoding a pesticidal polypeptide -

XX  
PS Claim 20; Page 55; 57pp; English.  
XX  
CC The present sequence is given in a specification which provides a  
CC recombinant host transformed with a polynucleotide encoding a pesticidal  
CC polypeptide. The polypeptide is neuropeptide F (NPF), or its functional  
CC equivalent, or trypsin modulating oostatic factor (TMOF), or a TMOF  
CC receptor-binding compound. The transformed host may be applied to a  
CC pest-inhabited area in order to control pests such as mosquitoes, flesh  
CC flies, fleas, sand flies, house flies and dog flies. The presence of a  
CC transformed host in the environment may be monitored by providing a host  
CC which has been transformed with a polynucleotide sequence which encodes  
CC a fluorescent compound. The pesticidal polypeptides are small in size  
CC and permit more rapid and efficient penetration into the midgut. They are  
CC also less expensive to produce by conventional chemical methods.  
XX  
SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 40

AAB26822

ID AAB26822 standard; peptide; 7 AA.

XX

AC AAB26822;

XX

DT 23-JAN-2001 (first entry)

XX

DE Peptidic membrane binding element.

XX

KW Organ perfusion; transplantation; storage; antiinflammatory;  
KW immunosuppressive; vasotropic; complement activation inhibitor;  
KW allograft rejection; ischaemia reperfusion injury.

XX

OS Synthetic.

XX

PN WO200053007-A1.

XX

PD 14-SEP-2000.

XX

PF 08-MAR-2000; 2000WO-GB00834.

XX

PR 10-MAR-1999; 99GB-0005503.

XX

PA (ADPR-) ADPROTECH LTD.

XX

PI Smith RAG, Pratt JR, Sacks SH;

XX

DR WPI; 2000-601920/57.

XX

PT Preparation for perfusing organ prior to transplantation or storage  
PT comprises soluble derivative of a soluble polypeptide which comprises  
PT two heterologous membrane binding elements with low membrane affinity  
PT -

XX

PS Example 2; Page 20; 47pp; English.

XX

CC The present invention relates to formulations and preparations for  
CC perfusing an organ prior to transplantation or storage. The preparation  
CC comprises a soluble derivative or a polypeptide, which has two or more  
CC heterologous membrane binding elements. The membrane binding elements are  
CC capable of interacting, independently and with thermodynamic additivity,  
CC with membrane components of the organ exposed to extracellular perfusion  
CC fluids, and a flush storage solution. The preparation exhibits  
CC antiinflammatory, immunosuppressive and vasotropic activity and works as  
CC a complement activation inhibitor and an inhibitor of cytotoxic T  
CC lymphocyte activity. The preparation is used for preparing an organ prior  
CC to transplantation or storage and for prevention, treatment or  
CC amelioration of a disease or disorder associated with inflammation,  
CC inappropriate complement activation or inappropriate activation of  
CC coagulant or thrombotic processes prior to, during or after  
CC transplantation or storage of an organ. The preparation is useful for  
CC treating hyperacute and acute allograft rejection of transplanted organs  
CC such as kidney, heart, liver or lungs, ischaemia-reperfusion injury in  
CC transplanted organs, xenograft rejection and corneal graft rejection. The  
CC present sequence represents a peptidic membrane binding element used in  
CC an example of the preparation of the invention.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4

|||

Db 3 SRL 5

RESULT 41

AAB17236

ID AAB17236 standard; Peptide; 7 AA.

XX

AC AAB17236;

XX

DT 31-OCT-2000 (first entry)

XX

DE SH3 antagonist peptide sequence SEQ ID NO:292.

XX

KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;  
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
KW vascular endothelial growth factor; matrix metalloproteinase;  
KW asthma; thrombosis; pharmaceutical.

XX

OS Synthetic.  
 XX  
 PN WO200024782-A2.  
 XX  
 PD 04-MAY-2000.  
 XX  
 PF 25-OCT-1999; 99WO-US25044.  
 XX  
 PR 23-OCT-1998; 98US-0105371.  
 PR 22-OCT-1999; 99US-0428082.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Feige U, Liu C, Cheetham J, Boone TC;  
 XX  
 DR WPI; 2000-350702/30.  
 XX  
 PT Novel composition of matter comprising an Fc domain and  
 PT pharmacologically active peptides, useful for treating cancer and  
 PT autoimmune diseases -  
 XX  
 PS Claim 39; Page 298; 608pp; English.  
 XX  
 CC The present invention describes composition of matter (I) comprising an  
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each  
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,  
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P<sup>3</sup>, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4  
 CC where P1, P2, P3, and P4 = are each independently sequences of  
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each  
 CC independently linkers; and a, b, c, d, e, and f = are each independently  
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can  
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive  
 CC activities. DNAs, vectors and host cells from the present invention can  
 CC be used for producing pharmaceutical compositions. The compositions are  
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.  
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer  
 CC half-life or incorporate functions such as Fc receptor binding, protein  
 CC A binding, complement fixation, and possibly placental transfer. AAA69443  
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid  
 CC sequences used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 1 SRL 3

RESULT 42  
 AAB12005  
 ID AAB12005 standard; peptide; 7 AA.  
 XX

AC AAB12005;  
 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 DE Brain homing peptide # 19.  
 XX  
 KW Brain; homing peptide; organ targeting; tissue targeting; mouse; cyclic.  
 XX  
 OS Mus sp.  
 XX  
 PN US6068829-A.  
 XX  
 PD 30-MAY-2000.  
 XX  
 PF 23-JUN-1997; 97US-0862855.  
 XX  
 PR 11-SEP-1995; 95US-0526710.  
 PR 10-MAR-1997; 97US-0813273.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Pasqualini R, Ruoslahti E;  
 XX  
 DR WPI; 2000-410850/35.  
 XX  
 PT Identifying and recovering organ homing molecules or peptides by in  
 PT vivo panning comprises administering a library of diverse peptides  
 PT linked to a tag which facilitates recovery of these peptides -  
 XX  
 PS Disclosure; Column 14; 20pp; English.  
 XX  
 CC The present sequence is a mouse brain homing peptide. This sequence was  
 CC identified by using in vivo panning to screen a library of potential  
 CC organ homing molecules. The present sequence can be used to direct a  
 CC moiety to a the brain tissue, by linking the moiety to the present  
 CC sequence. Examples of potential moieties are drugs, toxins or a  
 CC detectable label.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 3 SRL 5

RESULT 43  
 AAY94221  
 ID AAY94221 standard; Peptide; 7 AA.  
 XX  
 AC AAY94221;  
 XX  
 DT 08-AUG-2000 (first entry)  
 XX

DE Murine 16E10 light chain complementarily determining region 2.  
 XX  
 KW Antibody; RHAMM; receptor for hyaluronic acid mediated motility;  
 KW ras-dependent proliferation; leukaemia; cancer; lymphoma;  
 KW inflammatory disease; proliferative disease; psoriasis;  
 KW inflammatory bowel disease; rheumatoid arthritis;  
 KW proliferative cardiovascular disease; restenosis;  
 KW proliferative ocular disorder; diabetic retinopathy; haemangioma;  
 KW benign hyperproliferative disease; tumour formation; light chain;  
 KW variable region; 16E10; CDR2; complementarily determining region 2.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200029447-A1.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 19-NOV-1999; 99WO-US27565.  
 XX  
 PR 19-NOV-1998; 98US-0109041.  
 PR 14-JUL-1999; 99US-0143692.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Abrahamson JA, Holmes SD, Jackson JR;  
 XX  
 DR WPI; 2000-387752/33.  
 XX  
 PT Antibodies against receptor for hyaluronic acid mediated motility,  
 PT useful for treating or preventing proliferative diseases, e.g. cancer  
 PT or cardiovascular disease -  
 XX  
 PS Claim 23; Page 35; 39pp; English.  
 XX  
 CC The present sequence is the amino acid sequence for the murine 16E10  
 CC light chain complementarily determining region 2. This forms part of the  
 CC monoclonal antibody 16E10, which can be used against the receptor for  
 CC hyaluronic acid mediated motility (RHAMM). RHAMM is required for  
 CC ras-transformation of cells, which leads to tumour formation, and so the  
 CC antibody can be used to treat proliferative disorders such as leukaemias,  
 CC solid tumour cancers and metastases including lymphomas, soft tissue,  
 CC brain, oesophageal, stomach, pancreatic, liver, lung, bladder, bone,  
 CC prostate, ovarian, cervical, uterine, skin, breast, testicular, kidney,  
 CC head and neck and colon cancers, chronic inflammatory diseases such as  
 CC psoriasis, inflammatory bowel disease and rheumatoid arthritis,  
 CC proliferative cardiovascular diseases such as restenosis, proliferative  
 CC ocular disorders such as diabetic retinopathy and benign  
 CC hyperproliferative diseases such as haemangiomas.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db

|||  
3 SRL 5

RESULT 44

AAU72083

ID AAU72083 standard; Peptide; 7 AA.

XX

AC AAU72083;

XX

DT 26-FEB-2002 (first entry)

XX

DE Melanoma antigen, javelin peptide #69.

XX

KW Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;

KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYEs01; GM2;

KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;

KW javelin molecule; melanoma antigen recognised by T cells-1; human.

XX

OS Bacteriophage M13.

XX

PN WO200178655-A2.

XX

PD 25-OCT-2001.

XX

PF 17-APR-2001; 2001WO-US12449.

XX

PR 17-APR-2000; 2000US-197462P.

XX

PA (HOUG/) HOUGHTON A.

PA (LIVI/) LIVINGSTON P.

PA (ALAW/) AL-AWQATI Q.

PA (MAYH/) MAYHEW M.

PA (HOEM/) HOE M.

XX

PI Houghton A, Livingston P, Al-awqati Q, Mayhew M, Hoe M;

XX

DR WPI; 2001-663092/76.

XX

PT Anti cancer vaccine for the treatment of melanoma comprises a heat

PT shock protein and a melanoma antigen i.e. tyrosinase -

XX

PS Disclosure; Page 17; 150pp; English.

XX

CC The invention relates to a method of induction of an immune response,

CC comprising administration of an immunotherapeutic composition, comprising

CC a heat shock protein, and a melanoma antigen, where the melanoma

CC antigen is selected from tyrosinase, tyrosinase related protein 1,

CC tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens,

CC NYEs01, MART antigens, GM2, antigenic portions and combinations of these.

CC The melanoma antigen is covalently bound to a javelin molecule, where the

CC melanoma antigen bound to the javelin molecule is non-covalently bound to

CC the heat shock protein. The composition is useful for inducing an immune

CC response for the treatment of melanoma. AAU71980-AAU72481 represent

CC melanoma antigen peptides of the invention.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 45

AAE11811

ID AAE11811 standard; peptide; 7 AA.

XX

AC AAE11811;

XX

DT 18-DEC-2001 (first entry)

XX

DE Phage peptide #19 targetted to brain.

XX

KW Enriched library fraction; brain; kidney; tumour; panning; diagnostic;  
KW molecular medicine; drug delivery; peptidomimetic; pharmaceutical.

XX

OS Bacteriophage.

XX

PN US6296832-B1.

XX

PD 02-OCT-2001.

XX

PF 08-JAN-1999; 99US-0226985.

XX

PR 23-JUN-1997; 97US-0862855.

PR 11-SEP-1995; 95US-0526710.

PR 10-MAR-1997; 97US-0813273.

XX

PA (BURN-) BURNHAM INST.

XX

PI Ruoslahti E, Pasqualini R;

XX

DR WPI; 2001-610691/70.

XX

PT Enriched library fraction comprising molecules recovered by in vivo  
PT panning that selectively home to a selected organ or tissue useful for  
PT treating disease or in diagnostic methods -

XX

PS Disclosure; Column 14; 21pp; English.

XX

CC The invention relates to an enriched library fraction containing  
CC molecules that selectively home to a selected organ or tissue such as  
CC brain, kidney or tumour recovered by in vivo panning. The invention  
CC generally relates to the field of molecular medicine, drug delivery and  
CC to a method of invivo panning for identifying a molecule that homes to a  
CC specific organ. The molecules, e.g., peptides, peptidomimetics, proteins  
CC and fragments of proteins contained in an enriched library fraction may  
CC be administered to a subject as part of a pharmaceutical composition to  
CC treat disease or in diagnostic methods. The present sequence is a  
CC peptide from bacteriophage targetted to brain.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 3 SRL 5

RESULT 46

AAG63615

ID AAG63615 standard; peptide; 7 AA.

XX

AC AAG63615;

XX

DT 29-OCT-2001 (first entry)

XX

DE Complementarity determining region (CDR) 2 of ScFv1-1 H chain.

XX

KW Complementarity determining region; CDR; single chain antibody; ScFv;  
KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;  
KW envelope glycoprotein.

XX

OS Homo sapiens.

XX

PN WO200158459-A1.

XX

PD 16-AUG-2001.

XX

PF 13-FEB-2001; 2001WO-JP00967.

XX

PR 14-FEB-2000; 2000JP-0034906.

XX

PA (MITS-) MITSUBISHI-TOKYO PHARM INC.

XX

PI Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;

XX

DR WPI; 2001-496986/54.

XX

PT Remedies for hepatitis C containing substances with antiviral effects  
PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular  
PT compounds, by inhibiting binding of hepatitis C virus envelope  
PT glycoprotein or CD81 -

XX

PS Claim 18; Page 73; 138pp; Japanese.

XX

CC The present sequence represents a complementarity determining region  
CC (CDR) of a single chain (ScFv) antibody of the invention. The  
CC specification describes a substance can inhibit the binding between  
CC hepatitis C virus (HCV) and cells with potential HCV infection, cells  
CC with expression of CD81, or CD81. This substance is especially an  
CC antibody with affinity towards HCV E2/NS1 protein, containing amino  
CC acid sequences based on the CDR1, CDR2 and CDR3 of the H and L chain  
CC variable regions. The antibody inhibits the viral envelope glycoprotein.

CC It is also a CD81 inhibitor. The antibodies and drugs are used for  
CC treatment and/or prevention of hepatitis C, or for diagnosis of  
CC hepatitis C.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 3 SRL 5

#### RESULT 47

AAG63621

ID AAG63621 standard; peptide; 7 AA.

XX

AC AAG63621;

XX

DT 29-OCT-2001 (first entry)

XX

DE Complementarity determining region (CDR) 2 of ScFv1-3 H chain.

XX

KW Complementarity determining region; CDR; single chain antibody; ScFv;  
KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;  
KW envelope glycoprotein.

XX

OS Homo sapiens.

XX

PN WO200158459-A1.

XX

PD 16-AUG-2001.

XX

PF 13-FEB-2001; 2001WO-JP00967.

XX

PR 14-FEB-2000; 2000JP-0034906.

XX

PA (MITS-) MITSUBISHI-TOKYO PHARM INC.

XX

PI Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;

XX

DR WPI; 2001-496986/54.

XX

PT Remedies for hepatitis C containing substances with antiviral effects  
PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular  
PT compounds, by inhibiting binding of hepatitis C virus envelope  
PT glycoprotein or CD81 -

XX

PS Claim 22; Page 75; 138pp; Japanese.

XX

CC The present sequence represents a complementarity determining region  
CC (CDR) of a single chain (ScFv) antibody of the invention. The  
CC specification describes a substance can inhibit the binding between  
CC hepatitis C virus (HCV) and cells with potential HCV infection, cells  
CC with expression of CD81, or CD81. This substance is especially an

CC antibody with affinity towards HCV E2/NS1 protein, containing amino  
CC acid sequences based on the CDR1, CDR2 and CDR3 of the H and L chain  
CC variable regions. The antibody inhibits the viral envelope glycoprotein.  
CC It is also a CD81 inhibitor. The antibodies and drugs are used for  
CC treatment and/or prevention of hepatitis C, or for diagnosis of  
CC hepatitis C.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 3 SRL 5

#### RESULT 48

AAG98766

ID AAG98766 standard; peptide; 7 AA.

XX

AC AAG98766;

XX

DT 21-SEP-2001 (first entry)

XX

DE Human cell death protective cDNA clone CNI-00721 ORF19 peptide, SEQ:330.

XX

KW Cell death protective; apoptosis; necrosis; human; drug screening;  
KW cell death-associated disorder; central nervous system disorder;  
KW psychiatric disorder; neurological disorder; ischaemia-related disorder;  
KW stroke; cerebral infarction; ischaemic encephalopathy;  
KW neurodegenerative disorder; Alzheimer's disease; Huntington's disease;  
KW Parkinson's disease; infection; meningitis; malaria; trypanosomiasis;  
KW vascular disease; ophthalmological disorder; diabetic retinopathy;  
KW macular degeneration; hypertension; myocardial infarction;  
KW atherosclerosis; respiratory disorder; asthma; transgenic animal;  
KW chronic obstructive pulmonary disease; neoplastic condition; cancer;  
KW benign tumour; anaemia; gastrointestinal disorder; gastritis;  
KW ulcerative colitis; liver disease; biliary cirrhosis; kidney disorder;  
KW glomerulonephritis; cystitis; endometriosis; endocrine disorder;  
KW Grave's disease; Hashimoto's thyroiditis; skin condition; dermatitis;  
KW urticaria; immune disorder; acquired immunodeficiency syndrome; AIDS.

XX

OS Homo sapiens.

XX

PN WO200145638-A2.

XX

PD 28-JUN-2001.

XX

PF 11-DEC-2000; 2000WO-US33547.

XX

PR 14-DEC-1999; 99US-0461697.

XX

PA (COGE-) COGENT NEUROSCIENCE INC.

XX

PI Lo DC, Barney S, Thomas MB, Portbury SD, Puranam K, Katz LC;

XX  
DR WPI; 2001-390297/41.  
DR N-PSDB; AAH84281, AAH84300.  
XX  
PT Novel protective sequence polynucleotides and polypeptides, used to  
PT identify modulators of their expression and activity, which are used in  
PT to treat central nervous system conditions, diseases and disorders -  
XX  
PS Claim 1; Fig 11S; 325pp; English.  
XX  
CC Sequences AAH84132-AAH84370 represent human nucleic acid sequences which  
CC protect against cell death (i.e., apoptosis or necrosis). Sequences  
CC AAH84132, AAH84145, AAH84170, AAH84201, AAH84210, AAH84226, AAH84265,  
CC AAH84281, AAH84315 and AAH84367 represent 10 full-length cDNA clones,  
CC while the remaining nucleic acid sequences within the range given above  
CC represent the open reading frames (ORFs) of these cDNA clones. Sequences  
CC AAG98610-AAG98829 represent the polypeptides encoded by the cell death  
CC protective ORFs. The cell death protective cDNA clones are able to  
CC prevent, delay or reverse progression through the apoptotic or necrotic  
CC pathways when injected into a cell predisposed to or undergoing cell  
CC death. The cell death protective nucleic acids and polypeptides can be  
CC used in the diagnosis and treatment of disorders associated with cell  
CC death, and to screen for compounds which modulate their activity or  
CC expression. Such modulators, preferably a small organic molecule, an  
CC antibody, a ribozyme, or an antisense molecule, can also be used to treat  
CC cell death-related diseases. Such diseases include those associated with  
CC the central nervous system including psychiatric or neurological  
CC disorders, especially ischaemia-related conditions such as strokes, and  
CC also includes neurodegenerative disorders such as Alzheimer's disease,  
CC Huntington's disease, or Parkinson's disease. The modulators may also be  
CC used to treat infections such as meningitis, malaria, or trypanosomiasis;  
CC vascular diseases such as ischaemic encephalopathy or cerebral  
CC infarction; eye conditions such as diabetic retinopathy or macular  
CC degeneration; hypertension; myocardial infarction; atherosclerosis;  
CC respiratory conditions such as asthma or chronic obstructive pulmonary  
CC disease; neoplastic conditions such as cancers or benign tumours; blood  
CC cell conditions such as anaemia; gastrointestinal conditions such as  
CC gastritis or ulcerative colitis; liver conditions such as biliary  
CC cirrhosis; kidney disorders such as glomerulonephritis; cystitis;  
CC endometriosis; endocrine disorders such as Grave's disease or Hashimoto's  
CC thyroiditis; skin conditions such as dermatitis or urticaria; or immune  
CC system disorders such as acquired immunodeficiency syndrome (AIDS). The  
CC nucleic acids may additionally be used to generate animal models of  
CC cell death-associated disorders. The present sequence represents a  
CC cell death protective polypeptide.  
XX  
SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 4 SRL 6

RESULT 49

AAB84974

ID AAB84974 standard; protein; 7 AA.

XX

AC AAB84974;

XX

DT 06-AUG-2001 (first entry)

XX

DE Clone 2 scFv CDR L2 region binding to target antigen D.

XX

KW Antiinflammatory; antiallergic; cytostatic; antibacterial; antiviral;  
KW immunosuppressive; antidiabetic; neuroprotective; antirheumatic;  
KW antiarthritic; dermatological; immune response; modulator; enzyme;  
KW antigen D; T-cell receptor; complementary determining region; CDR.

XX

OS Homo sapiens.

XX

PN WO200140312-A2.

XX

PD 07-JUN-2001.

XX

PF 04-DEC-2000; 2000WO-GB04629.

XX

PR 03-DEC-1999; 99GB-0028789.

XX

PA (DIVE-) DIVERSYS LTD.

XX

PI Holt LJ, De Wildt RMT, Tomlinson I;

XX

DR WPI; 2001-374801/39.

XX

PT Isolating a polypeptide of interest from a naive polypeptide repertoire  
PT which has not been preselected with a specific target ligand involves  
PT direct screening of naive polypeptide repertoire with the target ligand  
PT -

XX

XX

PS Example 2; Page 29; 41pp; English.

XX

CC The invention relates to isolating, from a naive polypeptide (I)  
CC repertoire (antibody or T-cell receptor polypeptides), which has not been  
CC preselected with a specific target ligand, a polypeptide of interest (II)  
CC capable of interacting with the specific target ligand. The method  
CC involves direct screening of (I) with the target ligand in order to  
CC identify (II). The polypeptides selected by the method may be used in any  
CC process which involves ligand-polypeptide binding including in vivo  
CC therapeutic and prophylactic applications, in vitro and in vivo  
CC diagnostic applications, in vitro assay and reagent applications. Enzyme  
CC variants generated and selected by the method may be assayed for  
CC activity, either in vitro or in vivo using standard techniques. Antibody  
CC polypeptides selected by the method are used diagnostically in Western  
CC analysis and in situ protein detection. The selected antibodies are  
CC useful for preventing, suppressing or treating inflammatory states,  
CC allergic hypersensitivity, cancer, bacterial or viral infection and  
CC autoimmune disorders e.g., type I diabetes, multiple sclerosis,  
CC rheumatoid arthritis, systemic lupus erythematosus, Crohn's disease and  
CC myasthenia gravis. The selected polypeptides may be used extracorporeally  
CC or in vitro selectively to kill, deplete or effectively remove a target

CC cell population from a heterogeneous collection of cells. Sequences  
CC AAB84968-979 represent complementary determining regions (CDRs) of scFv  
CC heavy and light chains binding to target antigens M and D.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 3 SRL 5

#### RESULT 50

AAB84986

ID AAB84986 standard; peptide; 7 AA.

XX

AC AAB84986;

XX

DT 06-AUG-2001 (first entry)

XX

DE G12 scFv CDR L2 region binding to target antigen B.

XX

KW Antiinflammatory; antiallergic; cytostatic; antibacterial; antiviral;

KW immunosuppressive; antidiabetic; neuroprotective; antirheumatic;

KW antiarthritic; dermatological; immune response; modulator; enzyme;

KW antigen; T-cell receptor; complementary determining region; CDR.

XX

OS Homo sapiens.

XX

PN WO200140312-A2.

XX

PD 07-JUN-2001.

XX

PF 04-DEC-2000; 2000WO-GB04629.

XX

PR 03-DEC-1999; 99GB-0028789.

XX

PA (DIVE-) DIVERSYS LTD.

XX

PI Holt LJ, De Wildt RMT, Tomlinson I;

XX

DR WPI; 2001-374801/39.

XX

PT Isolating a polypeptide of interest from a naive polypeptide repertoire

PT which has not been preselected with a specific target ligand involves

PT direct screening of naive polypeptide repertoire with the target ligand

PT -

XX

PS Example 1; Fig 2; 41pp; English.

XX

CC The invention relates to isolating, from a naive polypeptide (I)

CC repertoire (antibody or T-cell receptor polypeptides), which has not been

CC preselected with a specific target ligand, a polypeptide of interest (II)

CC capable of interacting with the specific target ligand. The method



CC involves direct screening of (I) with the target ligand in order to  
CC identify (II). The polypeptides selected by the method may be used in any  
CC process which involves ligand-polypeptide binding including in vivo  
CC therapeutic and prophylactic applications, in vitro and in vivo  
CC diagnostic applications, in vitro assay and reagent applications. Enzyme  
CC variants generated and selected by the method may be assayed for  
CC activity, either in vitro or in vivo using standard techniques. Antibody  
CC polypeptides selected by the method are used diagnostically in Western  
CC analysis and in situ protein detection. The selected antibodies are  
CC useful for preventing, suppressing or treating inflammatory states,  
CC allergic hypersensitivity, cancer, bacterial or viral infection and  
CC autoimmune disorders e.g., type I diabetes, multiple sclerosis,  
CC rheumatoid arthritis, systemic lupus erythematosus, Crohn's disease and  
CC myasthenia gravis. The selected polypeptides may be used extracorporeally  
CC or in vitro selectively to kill, deplete or effectively remove a target  
CC cell population from a heterogeneous collection of cells. Sequences  
CC AAB84980-995 represent complementary determining regions (CDRs) of scFv  
CC heavy and light chains binding to target antigens M, B, C and O.  
XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

Search completed: November 28, 2003, 14:30:54  
Job time : 43 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:30:09 ; Search time 22 Seconds  
(without alignments)  
9.616 Million cell updates/sec

Title: US-09-228-866-45  
Perfect score: 5  
Sequence: 1 XSRLX 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 153337

Minimum DB seq length: 5  
Maximum DB seq length: 23

Post-processing: Listing first 100 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3	60.0	5	1	US-08-405-933-11	Sequence 11, Appl	
2	3	60.0	5	4	US-09-638-202A-41	Sequence 41, Appl	
3	3	60.0	5	4	US-09-638-202A-98	Sequence 98, Appl	
4	3	60.0	6	1	US-08-405-933-13	Sequence 13, Appl	
5	3	60.0	6	1	US-08-129-456A-19	Sequence 19, Appl	
6	3	60.0	6	2	US-08-350-260A-494	Sequence 494, App	
7	3	60.0	6	2	US-08-482-228-178	Sequence 178, App	
8	3	60.0	6	2	US-08-687-219B-10	Sequence 10, Appl	
9	3	60.0	6	3	US-08-482-528-178	Sequence 178, App	
10	3	60.0	6	3	US-08-360-821B-18	Sequence 18, Appl	
11	3	60.0	6	3	US-09-177-249-50	Sequence 50, Appl	

12	3	60.0	6	4	US-09-155-613A-92	Sequence 92, Appl
13	3	60.0	6	4	US-08-651-650-10	Sequence 10, Appl
14	3	60.0	6	4	US-09-104-337A-494	Sequence 494, App
15	3	60.0	7	1	US-08-526-710-19	Sequence 19, Appl
16	3	60.0	7	1	US-08-137-117D-118	Sequence 118, App
17	3	60.0	7	2	US-08-480-434-78	Sequence 78, Appl
18	3	60.0	7	2	US-08-436-717-118	Sequence 118, App
19	3	60.0	7	2	US-08-053-451B-78	Sequence 78, Appl
20	3	60.0	7	3	US-08-836-561-44	Sequence 44, Appl
21	3	60.0	7	3	US-08-328-239A-6	Sequence 6, Appli
22	3	60.0	7	3	US-08-862-855-19	Sequence 19, Appl
23	3	60.0	7	3	US-08-649-100-13	Sequence 13, Appl
24	3	60.0	7	3	US-08-649-100-29	Sequence 29, Appl
25	3	60.0	7	3	US-09-258-754-10	Sequence 10, Appl
26	3	60.0	7	3	US-09-258-754-170	Sequence 170, App
27	3	60.0	7	3	US-09-042-107-10	Sequence 10, Appl
28	3	60.0	7	3	US-09-042-107-170	Sequence 170, App
29	3	60.0	7	3	US-09-461-697-330	Sequence 330, App
30	3	60.0	7	3	US-09-226-985-19	Sequence 19, Appl
31	3	60.0	7	4	US-09-227-906-19	Sequence 19, Appl
32	3	60.0	7	4	US-09-434-122-44	Sequence 44, Appl
33	3	60.0	8	1	US-07-834-848-14	Sequence 14, Appl
34	3	60.0	8	2	US-08-669-284B-28	Sequence 28, Appl
35	3	60.0	8	2	US-08-482-228-27	Sequence 27, Appl
36	3	60.0	8	2	US-08-687-219B-3	Sequence 3, Appli
37	3	60.0	8	2	US-08-687-219B-4	Sequence 4, Appli
38	3	60.0	8	2	US-08-687-219B-5	Sequence 5, Appli
39	3	60.0	8	2	US-08-687-219B-6	Sequence 6, Appli
40	3	60.0	8	2	US-08-687-219B-7	Sequence 7, Appli
41	3	60.0	8	2	US-08-687-219B-8	Sequence 8, Appli
42	3	60.0	8	2	US-08-687-219B-19	Sequence 19, Appl
43	3	60.0	8	2	US-08-687-219B-20	Sequence 20, Appl
44	3	60.0	8	2	US-08-687-219B-21	Sequence 21, Appl
45	3	60.0	8	2	US-08-687-219B-22	Sequence 22, Appl
46	3	60.0	8	2	US-08-687-219B-23	Sequence 23, Appl
47	3	60.0	8	2	US-08-687-219B-24	Sequence 24, Appl
48	3	60.0	8	2	US-08-687-219B-35	Sequence 35, Appl
49	3	60.0	8	3	US-08-482-528-27	Sequence 27, Appl
50	3	60.0	8	3	US-08-925-002-24	Sequence 24, Appl
51	3	60.0	8	3	US-08-817-177-3	Sequence 3, Appli
52	3	60.0	8	3	US-09-056-226-12	Sequence 12, Appl
53	3	60.0	8	4	US-09-266-764-11	Sequence 11, Appl
54	3	60.0	8	5	PCT-US95-12686-3	Sequence 3, Appli
55	3	60.0	9	1	US-08-526-710-1	Sequence 1, Appli
56	3	60.0	9	1	US-08-526-710-3	Sequence 3, Appli
57	3	60.0	9	1	US-08-526-710-5	Sequence 5, Appli
58	3	60.0	9	2	US-08-340-283-72	Sequence 72, Appl
59	3	60.0	9	2	US-08-340-283-85	Sequence 85, Appl
60	3	60.0	9	2	US-08-350-260A-491	Sequence 491, App
61	3	60.0	9	2	US-08-350-260A-492	Sequence 492, App
62	3	60.0	9	2	US-08-350-260A-493	Sequence 493, App
63	3	60.0	9	2	US-08-286-861-20	Sequence 20, Appl
64	3	60.0	9	3	US-08-159-339A-445	Sequence 445, App
65	3	60.0	9	3	US-08-159-339A-973	Sequence 973, App
66	3	60.0	9	3	US-08-328-239A-5	Sequence 5, Appli
67	3	60.0	9	3	US-08-862-855-1	Sequence 1, Appli
68	3	60.0	9	3	US-08-862-855-3	Sequence 3, Appli

69	3	60.0	9	3	US-08-862-855-5	Sequence 5, Appli
70	3	60.0	9	3	US-09-258-754-65	Sequence 65, Appl
71	3	60.0	9	3	US-09-177-249-49	Sequence 49, Appl
72	3	60.0	9	3	US-09-042-107-65	Sequence 65, Appl
73	3	60.0	9	3	US-09-226-985-1	Sequence 1, Appli
74	3	60.0	9	3	US-09-226-985-3	Sequence 3, Appli
75	3	60.0	9	3	US-09-226-985-5	Sequence 5, Appli
76	3	60.0	9	4	US-09-227-906-1	Sequence 1, Appli
77	3	60.0	9	4	US-09-227-906-3	Sequence 3, Appli
78	3	60.0	9	4	US-09-227-906-5	Sequence 5, Appli
79	3	60.0	9	4	US-09-104-337A-491	Sequence 491, App
80	3	60.0	9	4	US-09-104-337A-492	Sequence 492, App
81	3	60.0	9	4	US-09-104-337A-493	Sequence 493, App
82	3	60.0	9	4	US-09-670-456A-3	Sequence 3, Appli
83	3	60.0	9	4	US-09-670-456A-5	Sequence 5, Appli
84	3	60.0	9	4	US-09-344-040C-118	Sequence 118, App
85	3	60.0	9	4	US-09-341-982-24	Sequence 24, Appl
86	3	60.0	10	1	US-08-129-456A-30	Sequence 30, Appl
87	3	60.0	10	1	US-07-965-667A-3	Sequence 3, Appli
88	3	60.0	10	1	US-08-627-497-8	Sequence 8, Appli
89	3	60.0	10	2	US-08-556-597-163	Sequence 163, App
90	3	60.0	10	2	US-08-488-161-21	Sequence 21, Appl
91	3	60.0	10	2	US-08-902-623-60	Sequence 60, Appl
92	3	60.0	10	2	US-08-595-043A-73	Sequence 73, Appl
93	3	60.0	10	2	US-08-629-291A-26	Sequence 26, Appl
94	3	60.0	10	2	US-08-792-553-8	Sequence 8, Appli
95	3	60.0	10	2	US-08-658-335B-26	Sequence 26, Appl
96	3	60.0	10	3	US-09-273-685-21	Sequence 21, Appl
97	3	60.0	10	3	US-08-484-819-3	Sequence 3, Appli
98	3	60.0	10	3	US-08-765-856-15	Sequence 15, Appl
99	3	60.0	10	3	US-08-894-173-3	Sequence 3, Appli
100	3	60.0	10	3	US-08-817-177-12	Sequence 12, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-405-933-11

; Sequence 11, Application US/08405933

; Patent No. 5516889

; GENERAL INFORMATION:

; APPLICANT: Hollenberg, Morley D.

; APPLICANT: Matsoukas, John M.

; APPLICANT: Moore, Graham J.

; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: Washington & Prince Streets, P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: USA

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/405,933
;   FILING DATE:
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/080,643
;   FILING DATE:  21-JUN-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Dillahunty, Mary Ann
;   REGISTRATION NUMBER:  34,576
;   REFERENCE/DOCKET NUMBER:  028722-059
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415)854-7400
;   TELEFAX:  (415)854-8275
;   INFORMATION FOR SEQ ID NO:  11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  5 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  circular
;   MOLECULE TYPE:  peptide
US-08-405-933-11

```

```

Query Match          60.0%;  Score 3;  DB 1;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy      2 SRL 4
      |||
Db      1 SRL 3

```

# RESULT 2

US-09-638-202A-41

```

; Sequence 41, Application US/09638202A
; Patent No. 6462189
;   GENERAL INFORMATION:
;   APPLICANT: Koieda, Shohei
;   TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
;   NUMBER OF SEQUENCES: 118
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
;   STREET: 121 South Eighth Street, Ste. 1600
;   CITY: Minneapolis
;   STATE: MN
;   COUNTRY: USA
;   ZIP: 55402
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version 2.0b
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/638,202A
;   FILING DATE: 11-Aug-2000
;   PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: 09/096,749  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ann S. Viksnins  
 ; REGISTRATION NUMBER: 37,748  
 ; REFERENCE/DOCKET NUMBER: 109.034US1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (612) 373-6900  
 ; TELEFAX: (612) 339-3061  
 ; INFORMATION FOR SEQ ID NO: 41:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; FRAGMENT TYPE: internal  
 ; ORIGINAL SOURCE:  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
 US-09-638-202A-41

Query Match 60.0%; Score 3; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 1 SRL 3

### RESULT 3

US-09-638-202A-98

; Sequence 98, Application US/09638202A  
 ; Patent No. 6462189

#### GENERAL INFORMATION:

; APPLICANT: Koieda, Shohei  
 ; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 118  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
 ; STREET: 121 South Eighth Street, Ste. 1600  
 ; CITY: Minneapolis  
 ; STATE: MN  
 ; COUNTRY: USA  
 ; ZIP: 55402

#### COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ Version 2.0b

#### CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/638,202A  
 ; FILING DATE: 11-Aug-2000

#### PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/096,749

```

;          FILING DATE: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;          NAME: Ann S. Viksnins
;          REGISTRATION NUMBER: 37,748
;          REFERENCE/DOCKET NUMBER: 109.034US1
;    TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (612) 373-6900
;          TELEFAX: (612) 339-3061
;    INFORMATION FOR SEQ ID NO: 98:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 5 amino acids
;        TYPE: amino acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      HYPOTHETICAL: NO
;      ANTI-SENSE: NO
;      FRAGMENT TYPE: internal
;      ORIGINAL SOURCE:
;      SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-09-638-202A-98

```

```

Query Match          60.0%;  Score 3;  DB 4;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          2 SRL 4
            |||
Db          1 SRL 3

```

RESULT 4

US-08-405-933-13

```

; Sequence 13, Application US/08405933
; Patent No. 5516889
;  GENERAL INFORMATION:
;    APPLICANT: Hollenberg, Morley D.
;    APPLICANT: Matsoukas, John M.
;    APPLICANT: Moore, Graham J.
;    TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
;    NUMBER OF SEQUENCES: 50
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Burns, Doane, Swecker & Mathis
;      STREET: Washington & Prince Streets, P.O. Box 1404
;      CITY: Alexandria
;      STATE: Virginia
;      COUNTRY: USA
;      ZIP: 22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/405,933
;      FILING DATE:
;      CLASSIFICATION: 514

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /label= Xaa
; OTHER INFORMATION: /note= "Xaa is Acp."
US-08-405-933-13

```

```

Query Match          60.0%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
      |||
Db      1 SRL 3

```

# RESULT 5

US-08-129-456A-19

```

; Sequence 19, Application US/08129456A
; Patent No. 5641867
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Clauss, Matthias
; APPLICANT: Kao, Janet
; APPLICANT: Kayton, Mark
; APPLICANT: Libutti, Steven K.
; TITLE OF INVENTION: Endothelial-Monocyte Activating
; TITLE OF INVENTION: Polypeptide II: A Mediator Which
; TITLE OF INVENTION: Activates Host Response
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```



```

; SOFTWARE: PatentIn Release #1.0 Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,456A
; FILING DATE: 29-SEP-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 278 0400
; TELEFAX: 212 391 0526
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-129-456A-19

```

```

Query Match          60.0%; Score 3; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
      |||
Db      2 SRL 4

```

# RESULT 6

```

US-08-350-260A-494
; Sequence 494, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 494:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-494

```

```

Query Match          60.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
      |||
Db      4 SRL 6

```

```

RESULT 7
US-08-482-228-178
; Sequence 178, Application US/08482228
; Patent No. 5968753
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy

```

```

; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,228
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-228-178

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```

Query Match          60.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches    3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          2 SRL 4
            |||
Db          2 SRL 4

```

# RESULT 8

US-08-687-219B-10

; Sequence 10, Application US/08687219B

; Patent No. 5985541

; GENERAL INFORMATION:

; APPLICANT: JOLIVET-REYNAUD, Colette

; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY

; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C VIRUS

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE, PLC

```

; STREET: 700 South Washington Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,219B
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 09005
; FILING DATE: 25-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38526
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal or C-terminal or internal
US-08-687-219B-10

```

```

Query Match          60.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches    3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      2 SRL 4
      |||
Db      4 SRL 6

```

# RESULT 9

```

US-08-482-528-178
; Sequence 178, Application US/08482528
; Patent No. 6017719
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgerson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.

```

```

; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,528
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-482-528-178

```

```

Query Match          60.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 SRL 4
      |||
Db      2 SRL 4

```

# RESULT 10

```

US-08-360-821B-18
; Sequence 18, Application US/08360821B
; Patent No. 6228837
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Clauss, Matthias
; APPLICANT: Kao, Janet
; APPLICANT: Kayton, Mark
; APPLICANT: Libutti, Steven K
; TITLE OF INVENTION: Endothelial Monocyte Activating
; TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host
Response
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham, LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York

```

```

; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821B
; FILING DATE: 08-OCT-96
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-360-821B-18

```

```

Query Match          60.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      2 SRL 4
        |||
Db      2 SRL 4

```

# RESULT 11

```

US-09-177-249-50
; Sequence 50, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324

```

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 50  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-177-249-50

Query Match 60.0%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 12

US-09-155-613A-92  
; Sequence 92, Application US/09155613A  
; Patent No. 6420120  
; GENERAL INFORMATION:  
; APPLICANT: Boulanger, Pierre  
; APPLICANT: Hong, Saw See  
; APPLICANT: Karayan, Lucie  
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses  
; FILE REFERENCE: 032751-036  
; CURRENT APPLICATION NUMBER: US/09/155,613A  
; CURRENT FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: PCT/FR98/00184  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: FR 97/01005  
; PRIOR FILING DATE: 1997-01-30  
; PRIOR APPLICATION NUMBER: FR 97/11166  
; PRIOR FILING DATE: 1997-09-09  
; NUMBER OF SEQ ID NOS: 98  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 92  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Phagotope  
US-09-155-613A-92

Query Match 60.0%; Score 3; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 1 SRL 3

RESULT 13

US-08-651-650-10  
; Sequence 10, Application US/08651650  
; Patent No. 6436903

```

; GENERAL INFORMATION:
;   APPLICANT:  CLAYBERGER, Carol A.
;   APPLICANT:  KRENSKY, Alan M.
;   TITLE OF INVENTION:  IMMUNOMODULATING COMPOUNDS COMPRISING
;   TITLE OF INVENTION:  D-ISOMERS OF AMINO ACIDS
;   NUMBER OF SEQUENCES:  38
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  MORRISON & FOERSTER
;     STREET:    2000 PENNSYLVANIA AVENUE, NW
;     CITY:     WASHINGTON
;     STATE:    DC
;     COUNTRY:   USA
;     ZIP:      20006-1888
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:    IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:    PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/651,650
;     FILING DATE:      22-MAY-1996
;     CLASSIFICATION:   536
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  MURASHIGE, KATE H.
;     REGISTRATION NUMBER:  29,959
;     REFERENCE/DOCKET NUMBER:  28600-20203.00
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (202) 887-1500
;     TELEFAX:   (202) 822-0168
;     TELEX:     90-4030
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  6 amino acids
;       TYPE:    amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  4
;     OTHER INFORMATION:  /note= "D-Leu"
US-08-651-650-10

```

```

Query Match          60.0%;  Score 3;  DB 4;  Length 6;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy          2 SRL 4
           |||
Db          1 SRL 3

```

```

RESULT 14
US-09-104-337A-494
; Sequence 494, Application US/09104337A
; Patent No. 6492160
;   GENERAL INFORMATION:
;     APPLICANT:  Winter, Gregory Paul

```



```

; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 494:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 494:
US-09-104-337A-494

```

```

Query Match          60.0%;  Score 3;  DB 4;  Length 6;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||

Db 4 SRL 6

RESULT 15

US-08-526-710-19

; Sequence 19, Application US/08526710

; Patent No. 5622699

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: Method of Identifying Molecules That

; TITLE OF INVENTION: Home to a Selected Organ In Vivo

; NUMBER OF SEQUENCES: 44

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell and Flores

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/526,710

; FILING DATE: 11-SEP-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-LJ 1779

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-526-710-19

Query Match 60.0%; Score 3; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 3 SRL 5

RESULT 16  
 US-08-137-117D-118  
 ; Sequence 118, Application US/08137117D  
 ; Patent No. 5795965  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TSUCHIYA, Masayuki  
 ; APPLICANT: SATO, Koh  
 ; APPLICANT: BENDIG, Mary  
 ; APPLICANT: JONES, Steven  
 ; APPLICANT: SALDANHA, Jose  
 ; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
 ; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR  
 ; NUMBER OF SEQUENCES: 158  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/137,117D  
 ; FILING DATE: 20-DEC-1993  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/JP92/00544  
 ; FILING DATE: 24-APR-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 4-32084  
 ; FILING DATE: 19-FEB-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 3-95476  
 ; FILING DATE: 25-APR-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: WEGNER, Harold C.  
 ; REGISTRATION NUMBER: 25,258  
 ; REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 118:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-137-117D-118

Query Match 60.0%; Score 3; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            2 SRL 4  
              |||  
Db            3 SRL 5

RESULT 17

US-08-480-434-78

; Sequence 78, Application US/08480434  
; Patent No. 5811248  
; GENERAL INFORMATION:  
; APPLICANT: Charles C. Ditlow, et al.  
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,  
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF  
; NUMBER OF SEQUENCES: 88  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,434  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Albert P. Halluin  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 7606-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 854-3660  
; TELEFAX: (415) 854-3694  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: N  
; ANTI-SENSE: N

US-08-480-434-78

Query Match                    60.0%; Score 3; DB 2; Length 7;  
Best Local Similarity    100.0%; Pred. No. 2.5e+05;  
Matches        3; Conservative    0; Mismatches    0; Indels        0; Gaps        0;

Qy            2 SRL 4  
              |||  
Db            3 SRL 5

RESULT 18

US-08-436-717-118

; Sequence 118, Application US/08436717

; Patent No. 5817790

; GENERAL INFORMATION:

; APPLICANT: TSUCHIYA, Masayuki

; APPLICANT: SATO, Koh

; APPLICANT: BENDIG, Mary

; APPLICANT: JONES, Steven

; APPLICANT: SALDANHA, Jose

; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR

; NUMBER OF SEQUENCES: 158

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/436,717

; FILING DATE:

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/137,117

; FILING DATE: 20-DEC-1993

; APPLICATION NUMBER: WO PCT/JP92/00544

; FILING DATE: 24-APR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 4-32084

; FILING DATE: 19-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 3-95476

; FILING DATE: 25-APR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: WEGNER, Harold C.

; REGISTRATION NUMBER: 25,258

; REFERENCE/DOCKET NUMBER: 53466/126/AAOK

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)672-5300

; TELEFAX: (202)672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 118:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-436-717-118

Query Match 60.0%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 19

US-08-053-451B-78

; Sequence 78, Application US/08053451B

; Patent No. 5955584

; GENERAL INFORMATION:

; APPLICANT: Chen, Francis W.

; APPLICANT: Ditlow, Charles C.

; APPLICANT: Calenoff, Emanuel

; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC

; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF

; NUMBER OF SEQUENCES: 176

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/053,451B

; FILING DATE: 26-APR-1993

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Halluin, Albert P.

; REGISTRATION NUMBER: 25,227

; REFERENCE/DOCKET NUMBER: 7606-033-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-854-3660

; TELEFAX: 415-854-3694

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 78:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: DNA

; HYPOTHETICAL: N

; ANTI-SENSE: N

US-08-053-451B-78

Query Match 60.0%; Score 3; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 20

US-08-836-561-44

; Sequence 44, Application US/08836561

; Patent No. 6018032

; GENERAL INFORMATION:

; APPLICANT: KOIKE, Masamichi

; APPLICANT: FURUYA, Akiko

; APPLICANT: NAKAMURA, Kazuyasu

; APPLICANT: IIDA, Akihiro

; APPLICANT: ANAZAWA, Hideharu

; APPLICANT: HANAI, No. 6018032uo

; APPLICANT: TAKATSU, Kiyoshi

; TITLE OF INVENTION: Antibody Against Human Interleukin-5

; TITLE OF INVENTION: Receptor Alpha Chain

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/836,561

; FILING DATE: 09-MAY-1997

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 232384/95

; FILING DATE: 11-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Lawrence, III, Stanton T

; REGISTRATION NUMBER: 25,736

; REFERENCE/DOCKET NUMBER: 7005-115-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090

; TELEFAX: 212-869-9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 44:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-836-561-44

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 21

US-08-328-239A-6

; Sequence 6, Application US/08328239A  
; Patent No. 6037136  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Galationov, Konstantin  
; APPLICANT: Jesus, Catherine  
; TITLE OF INVENTION: Interactions between Raf Proto-Oncogenes  
; TITLE OF INVENTION: and CDC25 Phosphatases, and Uses Related Thereto  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(Text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/328,239A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSV002.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1000  
; TELEFAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-328-239A-6

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 22

US-08-862-855-19

; Sequence 19, Application US/08862855  
; Patent No. 6068829  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Method of Identifying Molecules That  
; TITLE OF INVENTION: Home to a Selected Organ In Vivo  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/862,855  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/526,710  
; FILING DATE: 11-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/813,273  
; FILING DATE: 10-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 2621  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-862-855-19

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 23

US-08-649-100-13

; Sequence 13, Application US/08649100

; Patent No. 6114507

; GENERAL INFORMATION:

; APPLICANT: SHIRAKAWA, KAMON

; APPLICANT: MATUSUE, TOMOKAZU

; APPLICANT: NAGATA, SHIGEKAZU

; APPLICANT: CO, MAN SUNG

; APPLICANT: VASQUEZ, MAXIMILIANO

; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY

; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH

; STREET: PO BOX 747

; CITY: FALLS CHURCH

; STATE: VA

; COUNTRY: USA

; ZIP: 22040-0747

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/649,100

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: MURPHY JR, GERALD M

; REGISTRATION NUMBER: 28,977

; REFERENCE/DOCKET NUMBER: 1110-160

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 205-8000

; TELEFAX: (703) 205-8050

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-649-100-13

Query Match 60.0%; Score 3; DB 3; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 24

US-08-649-100-29

; Sequence 29, Application US/08649100  
; Patent No. 6114507  
; GENERAL INFORMATION:  
; APPLICANT: SHIRAKAWA, KAMON  
; APPLICANT: MATUSUE, TOMOKAZU  
; APPLICANT: NAGATA, SHIGEKAZU  
; APPLICANT: CO, MAN SUNG  
; APPLICANT: VASQUEZ, MAXIMILIANO  
; TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY  
; TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH  
; STREET: PO BOX 747  
; CITY: FALLS CHURCH  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/649,100  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURPHY JR, GERALD M  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1110-160  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

US-08-649-100-29

Query Match                    60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity       100.0%; Pred. No. 2.5e+05;  
Matches       3; Conservative       0; Mismatches       0; Indels       0; Gaps       0;  
  
Qy                    2 SRL 4  
                     |||  
Db                    3 SRL 5

RESULT 25

US-09-258-754-10  
 ; Sequence 10, Application US/09258754  
 ; Patent No. 6174687  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruoslahti, Erkki  
 ; APPLICANT: Pasqualini, Renata  
 ; APPLICANT: Rajotte, Daniel  
 ; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
 ; TITLE OF INVENTION: Membrane Dipeptidase  
 ; FILE REFERENCE: P-LJ 3443  
 ; CURRENT APPLICATION NUMBER: US/09/258,754  
 ; CURRENT FILING DATE: 1999-02-26  
 ; EARLIER APPLICATION NUMBER: 09/042,107  
 ; EARLIER FILING DATE: 1998-03-13  
 ; NUMBER OF SEQ ID NOS: 452  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-09-258-754-10

Query Match 60.0%; Score 3; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 4 SRL 6

RESULT 26  
 US-09-258-754-170  
 ; Sequence 170, Application US/09258754  
 ; Patent No. 6174687  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruoslahti, Erkki  
 ; APPLICANT: Pasqualini, Renata  
 ; APPLICANT: Rajotte, Daniel  
 ; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
 ; TITLE OF INVENTION: Membrane Dipeptidase  
 ; FILE REFERENCE: P-LJ 3443  
 ; CURRENT APPLICATION NUMBER: US/09/258,754  
 ; CURRENT FILING DATE: 1999-02-26  
 ; EARLIER APPLICATION NUMBER: 09/042,107  
 ; EARLIER FILING DATE: 1998-03-13  
 ; NUMBER OF SEQ ID NOS: 452  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 170  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-09-258-754-170

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 1 SRL 3

RESULT 27

US-09-042-107-10  
; Sequence 10, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-10

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 4 SRL 6

RESULT 28

US-09-042-107-170  
; Sequence 170, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 170  
; LENGTH: 7

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-170

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 1 SRL 3

RESULT 29

US-09-461-697-330

; Sequence 330, Application US/09461697  
; Patent No. 6277974  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Puranam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; TITLE OF INVENTION: CELL DEATH  
; FILE REFERENCE: 10001-005-999  
; CURRENT APPLICATION NUMBER: US/09/461,697  
; CURRENT FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 330  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-461-697-330

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 4 SRL 6

RESULT 30

US-09-226-985-19

; Sequence 19, Application US/09226985  
; Patent No. 6296832  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata

```

; TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-226-985-19

```

```

Query Match          60.0%; Score 3; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
      |||
Db      3 SRL 5

```

```

RESULT 31
US-09-227-906-19
; Sequence 19, Application US/09227906
; Patent No. 6306365
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki

```

```

; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-227-906-19

```

```

Query Match          60.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
      |||
Db      3 SRL 5

```

```

RESULT 32
US-09-434-122-44
; Sequence 44, Application US/09434122
; Patent No. 6538111

```



```

; GENERAL INFORMATION:
;   APPLICANT: KOIKE, Masamichi
;             FURUYA, Akiko
;             NAKAMURA, Kazuyasu
;             IIDA, Akihiro
;             ANAZAWA, Hideharu
;             HANAI, No. 6538111uo
;             TAKATSU, Kiyoshi
;   TITLE OF INVENTION: Antibody Against Human Interleukin-5
;                       Receptor Alpha Chain
;   NUMBER OF SEQUENCES: 106
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Pennie & Edmonds LLP
;     STREET: 1155 Avenue of the Americas
;     CITY: New York
;     STATE: NY
;     COUNTRY: USA
;     ZIP: 10036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/434,122
;     FILING DATE: 05-No. 6538111-1999
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/836,561
;     FILING DATE: 09-MAY-1997
;     APPLICATION NUMBER: JP 232384/95
;     FILING DATE: 11-SEP-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Lawrence, III, Stanton T
;     REGISTRATION NUMBER: 25,736
;     REFERENCE/DOCKET NUMBER: 7005-115-999
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 212-790-9090
;     TELEFAX: 212-869-9741
;     TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 44:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 7 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-434-122-44

```

```

Query Match          60.0%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
        |||
Db      3 SRL 5

```

RESULT 33  
 US-07-834-848-14  
 ; Sequence 14, Application US/07834848  
 ; Patent No. 5436221  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KITAGUCHI, HIROSHI  
 ; APPLICANT: KOMAZAWA, HIROYUKI  
 ; APPLICANT: KOJIMA, MASAYOSHI  
 ; APPLICANT: MORI, HIDETO  
 ; APPLICANT: NISHIKAWA, NAOYUKI  
 ; APPLICANT: SATOH, HIDEAKI  
 ; APPLICANT: ORIKASA, ATSUSHI  
 ; APPLICANT: ONO, MITSUNORI  
 ; APPLICANT: AZUMA, ICHIRO  
 ; APPLICANT: SAIKI, IKUO  
 ; TITLE OF INVENTION: PEPTIDE DERIVATIVES AND APPLICATION  
 ; TITLE OF INVENTION: THEREOF  
 ; NUMBER OF SEQUENCES: 18  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak, & Seas  
 ; STREET: 2100 Pennsylvania Ave., NW  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20037-3202  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/834,848  
 ; FILING DATE: 19920213  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Biggart, Waddell A.  
 ; REGISTRATION NUMBER: 24,861  
 ; REFERENCE/DOCKET NUMBER: Q28480  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)293-7060  
 ; TELEFAX: (202)293-7860  
 ; TELEX: 6491103  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: AMINO ACID  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-07-834-848-14

Query Match 60.0%; Score 3; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||

## RESULT 34

US-08-669-284B-28

; Sequence 28, Application US/08669284B

; Patent No. 5939534

## ; GENERAL INFORMATION:

; APPLICANT: Inoue, Makoto

; APPLICANT: Kikuchi, Kaoru

; APPLICANT: Ishige, Yoko

; APPLICANT: Ito, Akira

; APPLICANT: Kimura, Toru

; APPLICANT: Nakayama, Chikao

; APPLICANT: No. 5939534uchi, Hiroshi

; TITLE OF INVENTION: NOVEL HUMAN CILIARY NEUROTROPHIC FACTORS

; NUMBER OF SEQUENCES: 35

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK &amp; SEAS

; STREET: 2100 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20037

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/669,284B

; FILING DATE: 28-JUN-1996

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/JP94/02269

; FILING DATE: 27-DEC-1994

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 06-268281

; FILING DATE: 05-OCT-1994

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 06-201504

; FILING DATE: 02-AUG-1994

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 05-350934

; FILING DATE: 29-DEC-1993

## ; ATTORNEY/AGENT INFORMATION:

; NAME: Nakamura, Dean H.

; REGISTRATION NUMBER: 33,981

; REFERENCE/DOCKET NUMBER: Q-42041

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)293-7060

; TELEFAX: (202)293-7860

## ; INFORMATION FOR SEQ ID NO: 28:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide  
US-08-669-284B-28

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 6 SRL 8

RESULT 35

US-08-482-228-27

; Sequence 27, Application US/08482228

; Patent No. 5968753

; GENERAL INFORMATION:

; APPLICANT: Tseng-Law, Janet

; APPLICANT: Kobori, Joan A.

; APPLICANT: Al-Abdaly, Fahad A.

; APPLICANT: Guillermo, Roy

; APPLICANT: Helgerson, Sam L.

; APPLICANT: Deans, Robert J.

; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL

; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE

; NUMBER OF SEQUENCES: 215

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Janice Guthrie, Ph.D.

; STREET: P.O. Box 15210

; CITY: Irvine

; STATE: California

; COUNTRY: USA

; ZIP: 92713-5210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/482,228

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Guthrie, Janice

; REGISTRATION NUMBER: 35,170

; REFERENCE/DOCKET NUMBER: IT-4630CIP3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (714) 440-5353

; TELEFAX: (714) 553-1952

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-482-228-27

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 36

US-08-687-219B-3

; Sequence 3, Application US/08687219B

; Patent No. 5985541

; GENERAL INFORMATION:

; APPLICANT: JOLIVET-REYNAUD, Colette

; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY

; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C  
VIRUS

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE, PLC

; STREET: 700 South Washington Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/687,219B

; FILING DATE: 25-JUL-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95 09005

; FILING DATE: 25-JUL-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Berridge, William P.

; REGISTRATION NUMBER: 30,024

; REFERENCE/DOCKET NUMBER: WPB 38526

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703 836-6400

; TELEFAX: 703 836-2787

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal or C-terminal or internal

US-08-687-219B-3

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 6 SRL 8

RESULT 37

US-08-687-219B-4

; Sequence 4, Application US/08687219B

; Patent No. 5985541

; GENERAL INFORMATION:

; APPLICANT: JOLIVET-REYNAUD, Colette

; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY

; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C  
VIRUS

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE, PLC

; STREET: 700 South Washington Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/687,219B

; FILING DATE: 25-JUL-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95 09005

; FILING DATE: 25-JUL-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Berridge, William P.

; REGISTRATION NUMBER: 30,024

; REFERENCE/DOCKET NUMBER: WPB 38526

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703 836-6400

; TELEFAX: 703 836-2787

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal or C-terminal or internal

US-08-687-219B-4

Query Match 60.0%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 5 SRL 7

RESULT 38

US-08-687-219B-5

; Sequence 5, Application US/08687219B

; Patent No. 5985541

; GENERAL INFORMATION:

; APPLICANT: JOLIVET-REYNAUD, Colette

; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY

; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C VIRUS

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE, PLC

; STREET: 700 South Washington Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/687,219B

; FILING DATE: 25-JUL-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 95 09005

; FILING DATE: 25-JUL-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Berridge, William P.

; REGISTRATION NUMBER: 30,024

; REFERENCE/DOCKET NUMBER: WPB 38526

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703 836-6400

; TELEFAX: 703 836-2787

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal or C-terminal or internal

US-08-687-219B-5

Query Match 60.0%; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 4 SRL 6

RESULT 39

US-08-687-219B-6

; Sequence 6, Application US/08687219B

```

; Patent No. 5985541
; GENERAL INFORMATION:
;   APPLICANT: JOLIVET-REYNAUD, Colette
;   TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
;   TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C
VIRUS
;   NUMBER OF SEQUENCES: 40
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: OLIFF & BERRIDGE, PLC
;     STREET: 700 South Washington Street
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22314
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/687,219B
;     FILING DATE: 25-JUL-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: FR 95 09005
;     FILING DATE: 25-JUL-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Berridge, William P.
;     REGISTRATION NUMBER: 30,024
;     REFERENCE/DOCKET NUMBER: WPB 38526
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 703 836-6400
;     TELEFAX: 703 836-2787
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 8 amino acids
;       TYPE: amino acid
;       TOPOLOGY: unknown
;     MOLECULE TYPE: peptide
;     FRAGMENT TYPE: N-terminal or C-terminal or internal
US-08-687-219B-6

```

```

Query Match          60.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 SRL 4
      |||
Db      3 SRL 5

```

```

RESULT 40
US-08-687-219B-7
; Sequence 7, Application US/08687219B
; Patent No. 5985541
; GENERAL INFORMATION:
;   APPLICANT: JOLIVET-REYNAUD, Colette
;   TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY

```



; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C  
VIRUS  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OLIFF & BERRIDGE, PLC  
; STREET: 700 South Washington Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/687,219B  
; FILING DATE: 25-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 09005  
; FILING DATE: 25-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berridge, William P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 38526  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703 836-6400  
; TELEFAX: 703 836-2787  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal or C-terminal or internal  
US-08-687-219B-7

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
| | |  
Db 2 SRL 4

RESULT 41  
US-08-687-219B-8  
; Sequence 8, Application US/08687219B  
; Patent No. 5985541  
; GENERAL INFORMATION:  
; APPLICANT: JOLIVET-REYNAUD, Colette  
; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY  
; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C  
VIRUS  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: 700 South Washington Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,219B
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 09005
; FILING DATE: 25-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38526
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal or C-terminal or internal
US-08-687-219B-8

```

```

Query Match          60.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches    3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy          2 SRL 4
           |||
Db          1 SRL 3

```

```

RESULT 42
US-08-687-219B-19
; Sequence 19, Application US/08687219B
; Patent No. 5985541
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C
VIRUS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: 700 South Washington Street
; CITY: Alexandria
; STATE: VA

```

```

; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,219B
; FILING DATE: 25-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 09005
; FILING DATE: 25-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38526
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal or C-terminal or internal
US-08-687-219B-19

```

```

Query Match          60.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
      |||
Db      6 SRL 8

```

# RESULT 43

US-08-687-219B-20

```

; Sequence 20, Application US/08687219B
; Patent No. 5985541
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY
; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C
VIRUS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: 700 South Washington Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

;      COMPUTER:  PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/687,219B
;      FILING DATE:  25-JUL-1996
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 95 09005
;      FILING DATE:  25-JUL-1995
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Berridge, William P.
;      REGISTRATION NUMBER:  30,024
;      REFERENCE/DOCKET NUMBER:  WPB 38526
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703 836-6400
;      TELEFAX:  703 836-2787
;      INFORMATION FOR SEQ ID NO:  20:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;      MOLECULE TYPE:  peptide
;      FRAGMENT TYPE:  N-terminal or C-terminal or internal
US-08-687-219B-20

```

```

Query Match          60.0%;  Score 3;  DB 2;  Length 8;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          2  SRL 4
           |||
Db          5  SRL 7

```

```

RESULT 44
US-08-687-219B-21
; Sequence 21, Application US/08687219B
; Patent No. 5985541
; GENERAL INFORMATION:
; APPLICANT:  JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION:  PEPTIDE CAPABLE OF BEING RECOGNIZED BY
; TITLE OF INVENTION:  ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C
VIRUS
;      NUMBER OF SEQUENCES:  40
;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OLIFF & BERRIDGE, PLC
;      STREET:  700 South Washington Street
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22314
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/687,219B  
 ; FILING DATE: 25-JUL-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 95 09005  
 ; FILING DATE: 25-JUL-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Berridge, William P.  
 ; REGISTRATION NUMBER: 30,024  
 ; REFERENCE/DOCKET NUMBER: WPB 38526  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703 836-6400  
 ; TELEFAX: 703 836-2787  
 ; INFORMATION FOR SEQ ID NO: 21:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 8 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: N-terminal or C-terminal or internal  
 US-08-687-219B-21

Query Match 60.0%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 4 SRL 6

#### RESULT 45

US-08-687-219B-22

; Sequence 22, Application US/08687219B  
 ; Patent No. 5985541  
 ; GENERAL INFORMATION:  
 ; APPLICANT: JOLIVET-REYNAUD, Colette  
 ; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY  
 ; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C  
 VIRUS  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: OLIFF & BERRIDGE, PLC  
 ; STREET: 700 South Washington Street  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22314  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/687,219B  
 ; FILING DATE: 25-JUL-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: FR 95 09005

; FILING DATE: 25-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berridge, William P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 38526  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703 836-6400  
; TELEFAX: 703 836-2787  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal or C-terminal or internal  
US-08-687-219B-22

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 46

US-08-687-219B-23

; Sequence 23, Application US/08687219B  
; Patent No. 5985541  
; GENERAL INFORMATION:  
; APPLICANT: JOLIVET-REYNAUD, Colette  
; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY  
; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C  
VIRUS  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OLIFF & BERRIDGE, PLC  
; STREET: 700 South Washington Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/687,219B  
; FILING DATE: 25-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 09005  
; FILING DATE: 25-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berridge, William P.  
; REGISTRATION NUMBER: 30,024

; REFERENCE/DOCKET NUMBER: WPB 38526  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703 836-6400  
; TELEFAX: 703 836-2787  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal or C-terminal or internal  
US-08-687-219B-23

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 47

US-08-687-219B-24

; Sequence 24, Application US/08687219B  
; Patent No. 5985541  
; GENERAL INFORMATION:  
; APPLICANT: JOLIVET-REYNAUD, Colette  
; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY  
; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C  
VIRUS  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OLIFF & BERRIDGE, PLC  
; STREET: 700 South Washington Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/687,219B  
; FILING DATE: 25-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 09005  
; FILING DATE: 25-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berridge, William P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 38526  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703 836-6400  
; TELEFAX: 703 836-2787

; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal or C-terminal or internal  
US-08-687-219B-24

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 1 SRL 3

RESULT 48

US-08-687-219B-35

; Sequence 35, Application US/08687219B  
; Patent No. 5985541  
; GENERAL INFORMATION:  
; APPLICANT: JOLIVET-REYNAUD, Colette  
; TITLE OF INVENTION: PEPTIDE CAPABLE OF BEING RECOGNIZED BY  
; TITLE OF INVENTION: ANTIBODIES RECOGNIZING THE C33 ANTIGEN OF HEPATITIS C  
VIRUS

; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OLIFF & BERRIDGE, PLC  
; STREET: 700 South Washington Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/687,219B  
; FILING DATE: 25-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 95 09005  
; FILING DATE: 25-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berridge, William P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 38526  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703 836-6400  
; TELEFAX: 703 836-2787  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid



; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: N-terminal or C-terminal or internal  
US-08-687-219B-35

Query Match 60.0%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 4 SRL 6

RESULT 49

US-08-482-528-27

; Sequence 27, Application US/08482528  
; Patent No. 6017719  
; GENERAL INFORMATION:  
; APPLICANT: Tseng-Law, Janet  
; APPLICANT: Kobori, Joan A.  
; APPLICANT: Al-Abdaly, Fahad A.  
; APPLICANT: Guillermo, Roy  
; APPLICANT: Helgersen, Sam L.  
; APPLICANT: Deans, Robert J.  
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL  
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE  
; NUMBER OF SEQUENCES: 215  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janice Guthrie, Ph.D.  
; STREET: P.O. Box 15210  
; CITY: Irvine  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92713-5210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,528  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Guthrie, Janice  
; REGISTRATION NUMBER: 35,170  
; REFERENCE/DOCKET NUMBER: IT-4630CIP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 440-5353  
; TELEFAX: (714) 553-1952  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-482-528-27

Query Match 60.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 50

US-08-925-002-24

; Sequence 24, Application US/08925002  
; Patent No. 6048527  
; GENERAL INFORMATION:  
; APPLICANT: Granoff, Dan M.  
; APPLICANT: Moe, Gregory R.  
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE  
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE  
; TITLE OF INVENTION: COMPOSITIONS  
; FILE REFERENCE: 1238.002  
; CURRENT APPLICATION NUMBER: US/08/925,002  
; CURRENT FILING DATE: 1997-08-27  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sequence from  
; OTHER INFORMATION: a phage display peptide library

US-08-925-002-24

Query Match 60.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

Search completed: November 28, 2003, 14:33:11  
Job time : 23 secs

OM protein - protein search, using sw model

Run on: November 28, 2003, 14:32:09 ; Search time 30 Seconds  
 (without alignments)  
 30.741 Million cell updates/sec

Title: US-09-228-866-45  
 Perfect score: 5  
 Sequence: 1 XSRLX 5

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 143862

Minimum DB seq length: 5  
 Maximum DB seq length: 23

Post-processing: Listing first 100 summaries

Database : Published\_Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Score	Match Length	DB	ID	Description
No.					

1	3	60.0	5	9	US-09-096-749A-41	Sequence 41, Appl
2	3	60.0	5	9	US-09-096-749A-98	Sequence 98, Appl
3	3	60.0	5	11	US-09-903-412-41	Sequence 41, Appl
4	3	60.0	5	11	US-09-903-412-98	Sequence 98, Appl
5	3	60.0	5	12	US-10-165-155-41	Sequence 41, Appl
6	3	60.0	5	12	US-10-165-155-98	Sequence 98, Appl
7	3	60.0	5	12	US-10-190-162-41	Sequence 41, Appl
8	3	60.0	5	12	US-10-190-162-98	Sequence 98, Appl
9	3	60.0	5	12	US-10-302-817A-36	Sequence 36, Appl
10	3	60.0	5	15	US-10-103-327-31	Sequence 31, Appl
11	3	60.0	5	15	US-10-174-717A-41	Sequence 41, Appl
12	3	60.0	5	15	US-10-174-717A-98	Sequence 98, Appl
13	3	60.0	6	10	US-09-900-530A-34	Sequence 34, Appl
14	3	60.0	6	10	US-09-071-838-50	Sequence 50, Appl
15	3	60.0	6	10	US-09-851-026-18	Sequence 18, Appl
16	3	60.0	6	14	US-10-156-820-92	Sequence 92, Appl
17	3	60.0	6	15	US-10-213-512-50	Sequence 50, Appl
18	3	60.0	7	9	US-09-989-789-1558	Sequence 1558, Ap
19	3	60.0	7	9	US-09-192-854-16	Sequence 16, Appl
20	3	60.0	7	9	US-09-192-854-43	Sequence 43, Appl
21	3	60.0	7	9	US-09-192-854-88	Sequence 88, Appl
22	3	60.0	7	9	US-09-192-854-101	Sequence 101, App
23	3	60.0	7	9	US-09-192-854-126	Sequence 126, App
24	3	60.0	7	9	US-09-192-854-130	Sequence 130, App
25	3	60.0	7	9	US-09-192-854-145	Sequence 145, App
26	3	60.0	7	10	US-09-922-261-330	Sequence 330, App
27	3	60.0	7	10	US-09-968-561A-23	Sequence 23, Appl
28	3	60.0	7	10	US-09-968-561A-65	Sequence 65, Appl
29	3	60.0	7	10	US-09-968-561A-113	Sequence 113, App
30	3	60.0	7	10	US-09-968-561A-155	Sequence 155, App
31	3	60.0	7	10	US-09-968-561A-161	Sequence 161, App
32	3	60.0	7	10	US-09-968-561A-167	Sequence 167, App
33	3	60.0	7	10	US-09-968-561A-173	Sequence 173, App
34	3	60.0	7	10	US-09-968-561A-179	Sequence 179, App
35	3	60.0	7	10	US-09-968-561A-203	Sequence 203, App
36	3	60.0	7	10	US-09-968-561A-227	Sequence 227, App
37	3	60.0	7	10	US-09-968-561A-233	Sequence 233, App
38	3	60.0	7	10	US-09-968-561A-257	Sequence 257, App
39	3	60.0	7	10	US-09-996-288-123	Sequence 123, App
40	3	60.0	7	11	US-09-977-797A-34	Sequence 34, Appl
41	3	60.0	7	11	US-09-977-797A-42	Sequence 42, Appl
42	3	60.0	7	11	US-09-990-186-1558	Sequence 1558, Ap
43	3	60.0	7	11	US-09-563-222-39	Sequence 39, Appl
44	3	60.0	7	11	US-09-996-265-123	Sequence 123, App
45	3	60.0	7	11	US-09-954-385-18	Sequence 18, Appl
46	3	60.0	7	11	US-09-989-994-1558	Sequence 1558, Ap
47	3	60.0	7	12	US-10-052-578-211	Sequence 211, App
48	3	60.0	7	12	US-09-968-744A-23	Sequence 23, Appl
49	3	60.0	7	12	US-09-968-744A-65	Sequence 65, Appl
50	3	60.0	7	12	US-09-968-744A-113	Sequence 113, App
51	3	60.0	7	12	US-09-968-744A-155	Sequence 155, App
52	3	60.0	7	12	US-09-968-744A-161	Sequence 161, App
53	3	60.0	7	12	US-09-968-744A-167	Sequence 167, App
54	3	60.0	7	12	US-09-968-744A-173	Sequence 173, App
55	3	60.0	7	12	US-09-968-744A-179	Sequence 179, App
56	3	60.0	7	12	US-09-968-744A-203	Sequence 203, App

57	3	60.0	7	12	US-09-968-744A-227	Sequence 227, App
58	3	60.0	7	12	US-09-968-744A-233	Sequence 233, App
59	3	60.0	7	12	US-09-968-744A-257	Sequence 257, App
60	3	60.0	7	12	US-10-203-754A-5	Sequence 5, Appli
61	3	60.0	7	12	US-10-203-754A-11	Sequence 11, Appl
62	3	60.0	7	12	US-10-053-520-211	Sequence 211, App
63	3	60.0	7	12	US-10-053-498B-211	Sequence 211, App
64	3	60.0	7	14	US-10-140-555-9	Sequence 9, Appli
65	3	60.0	7	15	US-10-283-349-44	Sequence 44, Appl
66	3	60.0	8	10	US-09-017-743C-95	Sequence 95, Appl
67	3	60.0	8	10	US-09-910-552-24	Sequence 24, Appl
68	3	60.0	8	11	US-09-726-470A-127	Sequence 127, App
69	3	60.0	8	11	US-09-726-470A-235	Sequence 235, App
70	3	60.0	8	12	US-10-062-587-2	Sequence 2, Appli
71	3	60.0	8	12	US-10-190-082-370	Sequence 370, App
72	3	60.0	8	12	US-09-833-203-48	Sequence 48, Appl
73	3	60.0	8	12	US-10-160-162-264	Sequence 264, App
74	3	60.0	8	12	US-09-820-649-264	Sequence 264, App
75	3	60.0	8	12	US-10-137-867-42	Sequence 42, Appl
76	3	60.0	8	15	US-10-209-323-27	Sequence 27, Appl
77	3	60.0	8	15	US-10-147-910-10	Sequence 10, Appl
78	3	60.0	9	10	US-09-364-597A-20	Sequence 20, Appl
79	3	60.0	9	10	US-09-071-838-49	Sequence 49, Appl
80	3	60.0	9	10	US-09-824-787B-87	Sequence 87, Appl
81	3	60.0	9	10	US-09-824-787B-104	Sequence 104, App
82	3	60.0	9	10	US-09-840-277-61	Sequence 61, Appl
83	3	60.0	9	11	US-09-876-904A-471	Sequence 471, App
84	3	60.0	9	12	US-09-932-165-896	Sequence 896, App
85	3	60.0	9	12	US-09-932-165-1035	Sequence 1035, Ap
86	3	60.0	9	12	US-10-190-082-377	Sequence 377, App
87	3	60.0	9	12	US-10-190-082-463	Sequence 463, App
88	3	60.0	9	12	US-10-190-082-576	Sequence 576, App
89	3	60.0	9	12	US-09-833-203-49	Sequence 49, Appl
90	3	60.0	9	12	US-10-210-148-37	Sequence 37, Appl
91	3	60.0	9	12	US-10-210-148-91	Sequence 91, Appl
92	3	60.0	9	12	US-09-833-039-118	Sequence 118, App
93	3	60.0	9	12	US-10-306-878-11	Sequence 11, Appl
94	3	60.0	9	12	US-10-177-277-118	Sequence 118, App
95	3	60.0	9	12	US-10-277-292-38	Sequence 38, Appl
96	3	60.0	9	12	US-10-277-292-248	Sequence 248, App
97	3	60.0	9	12	US-10-277-292-329	Sequence 329, App
98	3	60.0	9	12	US-10-277-292-572	Sequence 572, App
99	3	60.0	9	12	US-10-280-340-38	Sequence 38, Appl
100	3	60.0	9	12	US-10-280-340-248	Sequence 248, App

#### ALIGNMENTS

#### RESULT 1

US-09-096-749A-41

; Sequence 41, Application US/09096749A

; Patent No. US20020019517A1

; GENERAL INFORMATION:

; APPLICANT: Koieda, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; NUMBER OF SEQUENCES: 118

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Schwegman, Lundberg, Woessner & Kluth P.A.
;   STREET:    121 South Eighth Street, Ste. 1600
;   CITY:      Minneapolis
;   STATE:     MN
;   COUNTRY:   USA
;   ZIP:       55402
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette
;   COMPUTER:    IBM Compatible
;   OPERATING SYSTEM:  DOS
;   SOFTWARE:    FastSEQ Version 2.0b
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/096,749A
;   FILING DATE:    June 12, 1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Ann S. Viksnins
;   REGISTRATION NUMBER:  37,748
;   REFERENCE/DOCKET NUMBER:  109.034US1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (612) 373-6900
;   TELEFAX:   (612) 339-3061
;   INFORMATION FOR SEQ ID NO:  41:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  5 amino acids
;   TYPE:    amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:    NO
;   FRAGMENT TYPE:  internal
;   ORIGINAL SOURCE:
US-09-096-749A-41

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Query Match          60.0%;  Score 3;  DB 9;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

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Qy      2  SRL 4
        |||
Db      1  SRL 3

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## RESULT 2

US-09-096-749A-98

```

; Sequence 98, Application US/09096749A
; Patent No. US20020019517A1
;   GENERAL INFORMATION:
;   APPLICANT:  Koieda, Shohei
;   TITLE OF INVENTION:  ARTIFICIAL ANTIBODY POLYPEPTIDES
;   NUMBER OF SEQUENCES:  118
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Schwegman, Lundberg, Woessner & Kluth P.A.

```

```

; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-09-096-749A-98

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Query Match          60.0%; Score 3; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches    3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

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Qy          2 SRL 4
            |||
Db          1 SRL 3

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# RESULT 3

```

US-09-903-412-41
; Sequence 41, Application US/09903412
; Publication No. US20030027319A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; FILE REFERENCE: 109.050US1
; CURRENT APPLICATION NUMBER: US/09/903,412
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/217,474
; PRIOR FILING DATE: 2000-07-11

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; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 41  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The sequence of the BC loop of ubiquitin-binding  
; OTHER INFORMATION: monobody clone 411.  
US-09-903-412-41

Query Match 60.0%; Score 3; DB 11; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 1 SRL 3

#### RESULT 4

US-09-903-412-98  
; Sequence 98, Application US/09903412  
; Publication No. US20030027319A1  
; GENERAL INFORMATION:  
; APPLICANT: Koide, Shohei  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; FILE REFERENCE: 109.050US1  
; CURRENT APPLICATION NUMBER: US/09/903,412  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: US 60/217,474  
; PRIOR FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 98  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: The sequence of the BC loop of clone 1 from Table  
; OTHER INFORMATION: 7.  
US-09-903-412-98

Query Match 60.0%; Score 3; DB 11; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 1 SRL 3

#### RESULT 5

US-10-165-155-41  
; Sequence 41, Application US/10165155  
; Publication No. US20030134386A1  
; GENERAL INFORMATION:



```

; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
;     STREET: 121 South Eighth Street, Ste. 1600
;     CITY: Minneapolis
;     STATE: MN
;     COUNTRY: USA
;     ZIP: 55402
; COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/165,155
;     FILING DATE: 06-Jun-2002
; PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/096,749
;     FILING DATE: June 12, 1998
; ATTORNEY/AGENT INFORMATION:
;     NAME: Ann S. Viksnins
;     REGISTRATION NUMBER: 37,748
;     REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (612) 373-6900
;     TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 41:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 5 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FRAGMENT TYPE: internal
;     ORIGINAL SOURCE:
;     SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-165-155-41

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Query Match          60.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
        |||
Db      1 SRL 3

```

```

RESULT 6
US-10-165-155-98
; Sequence 98, Application US/10165155
; Publication No. US20030134386A1
; GENERAL INFORMATION:
;     APPLICANT: Koieda, Shohei

```

```

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/165,155
; FILING DATE: 06-Jun-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749
; FILING DATE: June 12, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-10-165-155-98

```

```

Query Match          60.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
      |||
Db      1 SRL 3

```

#### RESULT 7

US-10-190-162-41

; Sequence 41, Application US/10190162

; Publication No. US20030170753A1

; GENERAL INFORMATION:

; APPLICANT: Koieda, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

```

;      NUMBER OF SEQUENCES: 118
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
;          STREET: 121 South Eighth Street, Ste. 1600
;          CITY: Minneapolis
;          STATE: MN
;          COUNTRY: USA
;          ZIP: 55402
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: Diskette
;          COMPUTER: IBM Compatible
;          OPERATING SYSTEM: DOS
;          SOFTWARE: FastSEQ Version 2.0b
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/10/190,162
;          FILING DATE: 03-Jul-2002
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/09/096,749
;          FILING DATE: June 12, 1998
;      ATTORNEY/AGENT INFORMATION:
;          NAME: Ann S. Viksnins
;          REGISTRATION NUMBER: 37,748
;          REFERENCE/DOCKET NUMBER: 109.034US1
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (612) 373-6900
;          TELEFAX: (612) 339-3061
;      INFORMATION FOR SEQ ID NO: 41:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 5 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;          MOLECULE TYPE: peptide
;          HYPOTHETICAL: NO
;          ANTI-SENSE: NO
;          FRAGMENT TYPE: internal
;          ORIGINAL SOURCE:
;          SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-190-162-41

```

```

Query Match          60.0%;  Score 3;  DB 12;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 SRL 4
        |||
Db      1 SRL 3

```

#### RESULT 8

US-10-190-162-98

; Sequence 98, Application US/10190162

; Publication No. US20030170753A1

; GENERAL INFORMATION:

; APPLICANT: Koieda, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; NUMBER OF SEQUENCES: 118

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/190,162
; FILING DATE: 03-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749
; FILING DATE: June 12, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-10-190-162-98

```

```

Query Match          60.0%;  Score 3;  DB 12;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 SRL 4
      |||
Db      1 SRL 3

```

```

RESULT 9
US-10-302-817A-36
; Sequence 36, Application US/10302817A
; Publication No. US20030198978A1
; GENERAL INFORMATION:
; APPLICANT: ROZZELLE, James
; APPLICANT: BOLCHAKOVA, Elena
; TITLE OF INVENTION: THERMUS BROCKIANUS NUCLEIC ACID POLYMERASES
; FILE REFERENCE: 4768US

```

; CURRENT APPLICATION NUMBER: US/10/302,817A  
; CURRENT FILING DATE: 2002-11-22  
; PRIOR APPLICATION NUMBER: 60/334,434  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 36  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Thermus brockianus  
US-10-302-817A-36

Query Match 60.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 10  
US-10-103-327-31  
; Sequence 31, Application US/10103327  
; Publication No. US20030106095A1  
; GENERAL INFORMATION:  
; APPLICANT: GARGER, Stephen A.  
; APPLICANT: TURPEN, Thomas H.  
; APPLICANT: KUMAGAI, Monto H.  
; TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN  
; TITLE OF INVENTION: PLANTS BY TRANSIENT EXPRESSION  
; FILE REFERENCE: 008010087CPUS06  
; CURRENT APPLICATION NUMBER: US/10/103,327  
; CURRENT FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: US/09/993,059  
; PRIOR FILING DATE: 2001-11-13  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 31  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Tobacco mosaic virus  
US-10-103-327-31

Query Match 60.0%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 11  
US-10-174-717A-41  
; Sequence 41, Application US/10174717A  
; Publication No. US20030108948A1

```

;      APPLICANT: Koide, Shohei
;      TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
;      NUMBER OF SEQUENCES: 118
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
;          STREET: 121 South Eighth Street, St. 1600
;          CITY: Minneapolis
;          STATE: MN
;          COUNTRY: USA
;          ZIP: 55402
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: Diskette
;          COMPUTER: IBM Compatible
;          OPERATING SYSTEM: WINDOWS
;          SOFTWARE: FastSEQ Version 2.0b
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/10/174,717A
;          FILING DATE: 18-Jun-2002
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 09/096,749
;          FILING DATE: June 12, 1998
;          APPLICATION NUMBER: 60/049,410
;          FILING DATE: June 12, 1997
;      ATTORNEY/AGENT INFORMATION:
;          NAME: Ann S. Viksnins
;          REGISTRATION NUMBER: 37,748
;          REFERENCE/DOCKET NUMBER: 109.034US4
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (612) 373-6900
;          TELEFAX: (612) 339-3061
;      INFORMATION FOR SEQ ID NO: 41:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 5 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;          MOLECULE TYPE: peptide
;          HYPOTHETICAL: NO
;          ANTI-SENSE: NO
;          FRAGMENT TYPE: internal
;          ORIGINAL SOURCE:
;          SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-174-717A-41

```

```

Query Match          60.0%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
        |||
Db      1 SRL 3

```

```

RESULT 12
US-10-174-717A-98
; Sequence 98, Application US/10174717A
; Publication No. US20030108948A1

```

```

;      APPLICANT: Koide, Shohei
;      TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
;      NUMBER OF SEQUENCES: 118
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
;          STREET: 121 South Eighth Street, St. 1600
;          CITY: Minneapolis
;          STATE: MN
;          COUNTRY: USA
;          ZIP: 55402
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: Diskette
;          COMPUTER: IBM Compatible
;          OPERATING SYSTEM: WINDOWS
;          SOFTWARE: FastSEQ Version 2.0b
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/10/174,717A
;          FILING DATE: 18-Jun-2002
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 09/096,749
;          FILING DATE: June 12, 1998
;          APPLICATION NUMBER: 60/049,410
;          FILING DATE: June 12, 1997
;      ATTORNEY/AGENT INFORMATION:
;          NAME: Ann S. Viksnins
;          REGISTRATION NUMBER: 37,748
;          REFERENCE/DOCKET NUMBER: 109.034US4
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (612) 373-6900
;          TELEFAX: (612) 339-3061
;      INFORMATION FOR SEQ ID NO: 98:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 5 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: single
;              TOPOLOGY: linear
;          MOLECULE TYPE: peptide
;          HYPOTHETICAL: NO
;          ANTI-SENSE: NO
;          FRAGMENT TYPE: internal
;          ORIGINAL SOURCE:
;          SEQUENCE DESCRIPTION: SEQ ID NO: 98:
US-10-174-717A-98

```

```

Query Match          60.0%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          2 SRL 4
            |||
Db          1 SRL 3

```

```

RESULT 13
US-09-900-530A-34
; Sequence 34, Application US/09900530A
; Patent No. US20020128438A1

```

```
; GENERAL INFORMATION:
; APPLICANT: Seol, Dae-Wu
; APPLICANT: Billiar, Timothy R.
; TITLE OF INVENTION: DNA Cassette for the Production of
; TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins,
Tetracycline
; TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus Vector,
Their
; TITLE OF INVENTION: Combination and Use in Gene Therapy
; FILE REFERENCE: 5006-1-002
; CURRENT APPLICATION NUMBER: US/09/900,530A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: KR 2000-38441
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 6
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-900-530A-34
```

```
Query Match          60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      2 SRL 4
      |||
Db      2 SRL 4
```

#### RESULT 14

US-09-071-838-50

```
; Sequence 50, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```



; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,838  
; FILING DATE: 01-MAY-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-086100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-071-838-50

Query Match 60.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 15

US-09-851-026-18

; Sequence 18, Application US/09851026  
; Patent No. US20020160957A1

; GENERAL INFORMATION:

; APPLICANT: Stern, David M.  
; Clauss, Matthias  
; Kao, Janet  
; Kayton, Mark  
; Libutti, Steven K

; TITLE OF INVENTION: Endothelial Monocyte Activating  
; Polypeptide II: A Mediator Which Activates Host

Response

; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham, LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.30, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/851,026

```

; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,821
; FILING DATE: 08-OCT-96
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-851-026-18

```

```

Query Match          60.0%; Score 3; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
      |||
Db      2 SRL 4

```

# RESULT 16

```

US-10-156-820-92
; Sequence 92, Application US/10156820
; Publication No. US20020150558A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156,820
; CURRENT FILING DATE: 2002-06-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotope

```

US-10-156-820-92

Query Match 60.0%; Score 3; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 1 SRL 3

RESULT 17

US-10-213-512-50

; Sequence 50, Application US/10213512  
; Publication No. US20030110536A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; FILE REFERENCE: 023070-086110US  
; CURRENT APPLICATION NUMBER: US/10/213,512  
; CURRENT FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: US/09/177,206  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: US 09/071,838  
; PRIOR FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 50  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-10-213-512-50

Query Match 60.0%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 18

US-09-989-789-1558

; Sequence 1558, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1558  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-789-1558

Query Match 60.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 19

US-09-192-854-16  
; Sequence 16, Application US/09192854  
; Patent No. US20020068276A1  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Greg  
; APPLICANT: Tomlinson, Ian  
; TITLE OF INVENTION: Methods for Selecting Functional Peptides  
; FILE REFERENCE: 3789/72916  
; CURRENT APPLICATION NUMBER: US/09/192,854  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/066,729  
; EARLIER FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-192-854-16

Query Match 60.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 20

US-09-192-854-43  
; Sequence 43, Application US/09192854  
; Patent No. US20020068276A1

```
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-192-854-43
```

```
Query Match          60.0%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      2 SRL 4
        |||
Db      3 SRL 5
```

#### RESULT 21

```
US-09-192-854-88
; Sequence 88, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 88
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-192-854-88
```

```
Query Match          60.0%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      2 SRL 4
        |||
Db      3 SRL 5
```

#### RESULT 22

US-09-192-854-101  
 ; Sequence 101, Application US/09192854  
 ; Patent No. US20020068276A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Winter, Greg  
 ; APPLICANT: Tomlinson, Ian  
 ; TITLE OF INVENTION: Methods for Selecting Functional Peptides  
 ; FILE REFERENCE: 3789/72916  
 ; CURRENT APPLICATION NUMBER: US/09/192,854  
 ; CURRENT FILING DATE: 1998-11-17  
 ; EARLIER APPLICATION NUMBER: 60/066,729  
 ; EARLIER FILING DATE: 1997-11-21  
 ; NUMBER OF SEQ ID NOS: 212  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 101  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-192-854-101

Query Match 60.0%; Score 3; DB 9; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 3 SRL 5

RESULT 23  
 US-09-192-854-126  
 ; Sequence 126, Application US/09192854  
 ; Patent No. US20020068276A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Winter, Greg  
 ; APPLICANT: Tomlinson, Ian  
 ; TITLE OF INVENTION: Methods for Selecting Functional Peptides  
 ; FILE REFERENCE: 3789/72916  
 ; CURRENT APPLICATION NUMBER: US/09/192,854  
 ; CURRENT FILING DATE: 1998-11-17  
 ; EARLIER APPLICATION NUMBER: 60/066,729  
 ; EARLIER FILING DATE: 1997-11-21  
 ; NUMBER OF SEQ ID NOS: 212  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 126  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-192-854-126

Query Match 60.0%; Score 3; DB 9; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 3 SRL 5

RESULT 24

US-09-192-854-130

; Sequence 130, Application US/09192854  
; Patent No. US20020068276A1  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Greg  
; APPLICANT: Tomlinson, Ian  
; TITLE OF INVENTION: Methods for Selecting Functional Peptides  
; FILE REFERENCE: 3789/72916  
; CURRENT APPLICATION NUMBER: US/09/192,854  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/066,729  
; EARLIER FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 130  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-192-854-130

Query Match 60.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 25

US-09-192-854-145

; Sequence 145, Application US/09192854  
; Patent No. US20020068276A1  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Greg  
; APPLICANT: Tomlinson, Ian  
; TITLE OF INVENTION: Methods for Selecting Functional Peptides  
; FILE REFERENCE: 3789/72916  
; CURRENT APPLICATION NUMBER: US/09/192,854  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/066,729  
; EARLIER FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 145  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-192-854-145

Query Match 60.0%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 26

US-09-922-261-330  
; Sequence 330, Application US/09922261  
; Patent No. US20020111471A1  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Puranam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES  
INVOLVING  
; TITLE OF INVENTION: CELL DEATH  
; FILE REFERENCE: 10001-005-999  
; CURRENT APPLICATION NUMBER: US/09/922,261  
; CURRENT FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US/09/461,697  
; PRIOR FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 330  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-922-261-330

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 4 SRL 6

RESULT 27

US-09-968-561A-23  
; Sequence 23, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different  
Ligands  
; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20



```

; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-968-561A-23

```

```

Query Match          60.0%;  Score 3;  DB 10;  Length 7;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 SRL 4
        |||
Db      3 SRL 5

```

#### RESULT 28

```

US-09-968-561A-65
; Sequence 65, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-968-561A-65

```

```

Query Match          60.0%;  Score 3;  DB 10;  Length 7;
Best Local Similarity 100.0%;  Pred. No. 6e+05;

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||

Db 3 SRL 5

RESULT 29

US-09-968-561A-113  
; Sequence 113, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands  
; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 113  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-113

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||

Db 3 SRL 5

RESULT 30

US-09-968-561A-155  
; Sequence 155, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands  
; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A

; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 155  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-155

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 31  
US-09-968-561A-161  
; Sequence 161, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different  
Ligands  
; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 161  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-161

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 32

US-09-968-561A-167

; Sequence 167, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different  
Ligands

; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 167  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-167

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 33

US-09-968-561A-173

; Sequence 173, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory

```

; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 173
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-173

```

```

Query Match          60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
        |||
Db      3 SRL 5

```

#### RESULT 34

US-09-968-561A-179

```

; Sequence 179, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 179

```

; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-179

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 35

US-09-968-561A-203  
; Sequence 203, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different  
Ligands  
; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 203  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-203

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 36

US-09-968-561A-227  
; Sequence 227, Application US/09968561A  
; Patent No. US20020164642A1

```

; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 227
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-227

```

```

Query Match          60.0%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          2 SRL 4
            |||
Db          3 SRL 5

```

# RESULT 37

```

US-09-968-561A-233
; Sequence 233, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24

```

; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 233  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-233

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 38

US-09-968-561A-257  
; Sequence 257, Application US/09968561A  
; Patent No. US20020164642A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different  
Ligands  
; FILE REFERENCE: 8039/1073B  
; CURRENT APPLICATION NUMBER: US/09/968,561A  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 257  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-257

Query Match 60.0%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 39



US-09-996-288-123  
 ; Sequence 123, Application US/09996288  
 ; Patent No. US20020177126A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Young, James  
 ; APPLICANT: Scott, Koenig  
 ; APPLICANT: Leslie, Johnson  
 ; TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxis  
 ; TITLE OF INVENTION: and Treatment  
 ; FILE REFERENCE: 10271-047-999  
 ; CURRENT APPLICATION NUMBER: US/09/996,288  
 ; CURRENT FILING DATE: 2001-11-28  
 ; NUMBER OF SEQ ID NOS: 259  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 123  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-996-288-123

Query Match 60.0%; Score 3; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 3 SRL 5

RESULT 40  
 US-09-977-797A-34  
 ; Sequence 34, Application US/09977797A  
 ; Publication No. US20030044772A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Watkins, Jeffrey D.  
 ; APPLICANT: Huse, William D.  
 ; APPLICANT: Wu, Herren  
 ; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules  
 ; FILE REFERENCE: AME-06805  
 ; CURRENT APPLICATION NUMBER: US/09/977,797A  
 ; CURRENT FILING DATE: 2002-06-25  
 ; PRIOR APPLICATION NUMBER: 09/129,026  
 ; PRIOR FILING DATE: 1998-08-04  
 ; PRIOR APPLICATION NUMBER: 08/905,825  
 ; PRIOR FILING DATE: 1997-08-04  
 ; NUMBER OF SEQ ID NOS: 136  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 34  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-977-797A-34

Query Match 60.0%; Score 3; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 41

US-09-977-797A-42

; Sequence 42, Application US/09977797A

; Publication No. US20030044772A1

; GENERAL INFORMATION:

; APPLICANT: Watkins, Jeffrey D.

; APPLICANT: Huse, William D.

; APPLICANT: Wu, Herren

; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules

; FILE REFERENCE: AME-06805

; CURRENT APPLICATION NUMBER: US/09/977,797A

; CURRENT FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: 09/129,026

; PRIOR FILING DATE: 1998-08-04

; PRIOR APPLICATION NUMBER: 08/905,825

; PRIOR FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 136

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 42

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-977-797A-42

Query Match 60.0%; Score 3; DB 11; Length 7;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 42

US-09-990-186-1558

; Sequence 1558, Application US/09990186

; Publication No. US20030068675A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.21 / S11-US3

; CURRENT APPLICATION NUMBER: US/09/990,186

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1558

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-990-186-1558

Query Match 60.0%; Score 3; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 43

US-09-563-222-39

; Sequence 39, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 39  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus

US-09-563-222-39

Query Match 60.0%; Score 3; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 44

US-09-996-265-123

; Sequence 123, Application US/09996265  
; Publication No. US20030091584A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, James  
; APPLICANT: Scott, Koenig  
; APPLICANT: Leslie, Johnson  
; TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for  
Prophylaxis  
; TITLE OF INVENTION: and Treatment  
; FILE REFERENCE: 10271-048-999  
; CURRENT APPLICATION NUMBER: US/09/996,265  
; CURRENT FILING DATE: 2001-11-28  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 123  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-996-265-123

Query Match 60.0%; Score 3; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 45

US-09-954-385-18

; Sequence 18, Application US/09954385  
; Publication No. US20030100467A1  
; GENERAL INFORMATION:  
; APPLICANT: Aehle, Wolfgang  
; APPLICANT: Baldwin, Toby L.  
; APPLICANT: Van Gastel, Franciscus J.C.  
; APPLICANT: Janssen, Giselle G.  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Wang, Huaming  
; APPLICANT: Winetzky, Deborah S.  
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
; TITLE OF INVENTION: Complexes  
; FILE REFERENCE: GC690  
; CURRENT APPLICATION NUMBER: US/09/954,385  
; CURRENT FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 433  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: binding peptide  
US-09-954-385-18

Query Match 60.0%; Score 3; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 46

US-09-989-994-1558

; Sequence 1558, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang

```

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1558
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-994-1558

```

```

Query Match          60.0%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 SRL 4
        |||
Db      3 SRL 5

```

#### RESULT 47

```

US-10-052-578-211
; Sequence 211, Application US/10052578
; Publication No. US20030134787A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 211
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-052-578-211

```

```

Query Match          60.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

Qy 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 48

US-09-968-744A-23  
; Sequence 23, Application US/09968744A  
; Publication No. US20030148372A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different  
Ligands  
; FILE REFERENCE: 8039/1073  
; CURRENT APPLICATION NUMBER: US/09/968,744A  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-744A-23

Query Match 60.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 49

US-09-968-744A-65  
; Sequence 65, Application US/09968744A  
; Publication No. US20030148372A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different  
Ligands  
; FILE REFERENCE: 8039/1073  
; CURRENT APPLICATION NUMBER: US/09/968,744A  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: GB 9722131.1

; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 65  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-744A-65

Query Match 60.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

RESULT 50

US-09-968-744A-113  
; Sequence 113, Application US/09968744A  
; Publication No. US20030148372A1  
; GENERAL INFORMATION:  
; APPLICANT: Tomlinson, Ian M  
; APPLICANT: Winter, Gregory  
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different  
Ligands  
; FILE REFERENCE: 8039/1073  
; CURRENT APPLICATION NUMBER: US/09/968,744A  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: GB 9722131.1  
; PRIOR FILING DATE: 1997-10-20  
; PRIOR APPLICATION NUMBER: US 60/065,248  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: US 60/066,729  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: US 09/511,939  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 113  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-744A-113

Query Match 60.0%; Score 3; DB 12; Length 7;

Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 3 SRL 5

Search completed: November 28, 2003, 14:37:21  
Job time : 30 secs



OM protein - protein search, using sw model

Run on: November 28, 2003, 14:28:24 ; Search time 20 Seconds  
 (without alignments)  
 24.042 Million cell updates/sec

Title: US-09-228-866-45  
 Perfect score: 5  
 Sequence: 1 XSRLX 5

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4406

Minimum DB seq length: 5  
 Maximum DB seq length: 23

Post-processing: Listing first 100 summaries

Database : PIR\_76:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	%		Query Match	Length	DB	ID	Description
	Score						
1	3	60.0	11	2	PT0217	T-cell receptor be	
2	3	60.0	12	1	LFECPE	pyrE leader peptid	
3	3	60.0	15	2	PA0029	protein QA100012 -	
4	3	60.0	15	2	G41299	T-cell receptor al	
5	3	60.0	15	2	PH0770	T-cell receptor be	
6	3	60.0	16	2	S35627	uvsX protein - pha	
7	3	60.0	16	2	A28587	T-cell receptor be	
8	3	60.0	17	2	JP0068	ribosomal protein	
9	3	60.0	17	2	E28587	T-cell receptor be	
10	3	60.0	17	2	H53284	T-cell receptor be	
11	3	60.0	19	2	PC1324	hypothetical prote	
12	3	60.0	19	2	PC1322	hypothetical prote	
13	3	60.0	20	2	C20554	hemocyanin subunit	

14	3	60.0	20	2	I67551	monocyte chemotact
15	3	60.0	22	2	S35624	uvsX protein - pha
16	2	40.0	5	2	T14910	hypothetical prote
17	2	40.0	5	2	S53595	hypothetical prote
18	2	40.0	5	2	PT0525	T-cell receptor be
19	2	40.0	5	2	PT0577	T-cell receptor be
20	2	40.0	5	2	PT0565	T-cell receptor be
21	2	40.0	5	2	PT0700	T-cell receptor be
22	2	40.0	6	2	B33932	Ig mu chain D regi
23	2	40.0	6	2	PT0518	T-cell receptor be
24	2	40.0	6	2	PT0662	T-cell receptor be
25	2	40.0	7	2	S19630	ribosomal protein
26	2	40.0	7	2	ECMUCR	catch-relaxing pep
27	2	40.0	7	2	A15398	choline oxidase (E
28	2	40.0	7	2	PN0150	omega-gliadine 1'
29	2	40.0	7	2	A28340	myomodulin - Calif
30	2	40.0	7	2	PT0671	T-cell receptor be
31	2	40.0	7	2	PH0932	T-cell receptor be
32	2	40.0	8	1	LFSAME	probable msrA lead
33	2	40.0	8	2	PH1407	Ig heavy chain V r
34	2	40.0	8	2	T10077	hypothetical prote
35	2	40.0	8	2	PC4131	hypothetical prote
36	2	40.0	8	2	PL0162	paramyosin - north
37	2	40.0	8	2	A23967	leucopyrokinin - M
38	2	40.0	8	2	T13818	cytochrome oxidase
39	2	40.0	8	2	A59028	MHC class I histoc
40	2	40.0	9	2	B45796	dihydrolipoamide S
41	2	40.0	9	2	A61620	locustamyotropin I
42	2	40.0	9	2	S78762	ribosomal protein
43	2	40.0	9	2	S78420	ribosomal protein
44	2	40.0	10	2	B33710	ornithine decarbox
45	2	40.0	10	2	C39191	hypothetical prote
46	2	40.0	10	2	PC2044	beta-Kirilowin - M
47	2	40.0	10	2	S19296	16K protein - poul
48	2	40.0	10	2	PT0309	Ig heavy chain CRD
49	2	40.0	10	2	PT0212	T-cell receptor al
50	2	40.0	10	2	PH0894	T-cell receptor be
51	2	40.0	10	2	PH0926	T-cell receptor be
52	2	40.0	10	2	PH0895	T-cell receptor be
53	2	40.0	10	2	PC4374	telomeric and tetr
54	2	40.0	10	2	T17063	cytochrome-c oxida
55	2	40.0	11	2	A40693	transgelin - sheep
56	2	40.0	11	2	D58502	27K bile and gallb
57	2	40.0	11	2	S05002	corazonin - Americ
58	2	40.0	11	2	PT0273	Ig heavy chain CRD
59	2	40.0	11	2	S13279	Ile-Ser-bradykinin
60	2	40.0	11	2	PH1584	Ig H chain V-D-J r
61	2	40.0	11	2	PH0929	T-cell receptor be
62	2	40.0	11	2	PH0947	T-cell receptor be
63	2	40.0	11	2	PH0903	T-cell receptor be
64	2	40.0	11	2	PH0919	T-cell receptor be
65	2	40.0	11	4	I52708	ELAV-like neuronal
66	2	40.0	11	4	S41909	hypothetical prote
67	2	40.0	11	4	PC2124	aminotransferase c
68	2	40.0	12	1	A43975	locustamyotropin -
69	2	40.0	12	2	A29169	phospholipase A2 (
70	2	40.0	12	2	C49215	urease (EC 3.5.1.5

71	2	40.0	12	2	S26541	T-cell receptor be
72	2	40.0	12	2	S26555	T-cell receptor be
73	2	40.0	12	2	S26556	T-cell receptor be
74	2	40.0	12	2	S26554	T-cell receptor be
75	2	40.0	12	2	S36902	Em protein - wheat
76	2	40.0	12	2	A44874	proboscipedia - fr
77	2	40.0	12	2	S29859	gene p10 protein -
78	2	40.0	12	2	S71034	potB protein - Sal
79	2	40.0	12	2	D28551	hypothetical prote
80	2	40.0	12	2	S49547	hypothetical prote
81	2	40.0	12	2	A56878	light yellow cell
82	2	40.0	12	2	C61308	hemocyanin chain 6
83	2	40.0	12	2	A49637	MHC class II histo
84	2	40.0	12	2	A37933	Ig lambda chain J
85	2	40.0	12	2	C30503	Ig gamma-2b chain
86	2	40.0	12	2	PH1581	Ig H chain V-D-J r
87	2	40.0	12	2	PH0746	T-cell receptor be
88	2	40.0	12	2	A42324	cytochrome P450c27
89	2	40.0	12	2	PH0931	T-cell receptor be
90	2	40.0	12	2	S21163	NAD ADP-ribosyltra
91	2	40.0	13	2	A53608	neurotensin - guin
92	2	40.0	13	2	S78519	ribosomal protein
93	2	40.0	13	2	E39778	lactose phosphotra
94	2	40.0	13	2	JH0460	corticostatic pept
95	2	40.0	13	2	H44957	protein P18 - comm
96	2	40.0	13	2	B61620	locustamyotropin I
97	2	40.0	13	2	PT0256	Ig heavy chain CRD
98	2	40.0	13	2	PT0293	Ig heavy chain CRD
99	2	40.0	13	2	PT0304	Ig heavy chain CRD
100	2	40.0	13	2	S47359	T-cell antigen rec

# ALIGNMENTS

## RESULT 1

PT0217

T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C;Accession: PT0217

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0217

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 60.0%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 6.7e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db

3 SRL 5

RESULT 2

LFECPE

pyrE leader peptide - Escherichia coli

C;Species: Escherichia coli

C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 31-Mar-1993

C;Accession: A30400; A05110; Q00495

R;Poulsen, P.; Bonekamp, F.; Jensen, K.F.

EMBO J. 3, 1783-1790, 1984

A;Title: Structure of the Escherichia coli pyrE operon and control of pyrE expression by a UTP modulated intercistronic attenuation.

A;Reference number: A30400; MUID:85003588; PMID:6207018

A;Accession: A30400

A;Molecule type: DNA

A;Residues: 1-12 <POU1>

R;Poulsen, P.; Jensen, K.F.; Valentin-Hansen, P.; Carlsson, P.; Lundberg, L.G.  
Eur. J. Biochem. 135, 223-229, 1983

A;Title: Nucleotide sequence of the Escherichia coli pyrE gene and of the DNA in front of the protein-coding region.

A;Reference number: A05110; MUID:83287414; PMID:6349999

A;Accession: A05110

A;Molecule type: DNA

A;Residues: 1-12 <POU2>

C;Genetics:

A;Gene: pyrE-LP

A;Map position: 82 min

C;Superfamily: pyrE leader peptide

Query Match 60.0%; Score 3; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 7.2e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 2 SRL 4

RESULT 3

PA0029

protein QA100012 - Arabidopsis thaliana (fragment)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997

C;Accession: PA0029

R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis.

A;Reference number: PA0001

A;Accession: PA0029

A;Molecule type: protein

A;Residues: 1-15 <KAM>

A;Experimental source: callus

Query Match 60.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 4 SRL 6

RESULT 4

G41299

T-cell receptor alpha chain precursor J region (39) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 28-May-1992 #sequence\_revision 28-May-1992 #text\_change 05-Nov-1999

C;Accession: G41299

R;Uematsu, Y.; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G.; Steinmetz, M.

Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991

A;Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheumatoid arthritis is polyclonal.

A;Reference number: A41299; MUID:92020887; PMID:1656449

A;Accession: G41299

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-15 <UEM>

A;Cross-references: GB:S57457; NID:g236330; PIDN:AAB19962.1; PID:g236331

C;Keywords: T-cell receptor

Query Match 60.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 9 SRL 11

RESULT 5

PH0770

T-cell receptor beta chain (L4) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C;Accession: PH0770

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L. J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium berghei nonapeptide: implications for T cell allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0770

A;Molecule type: mRNA

A;Residues: 1-15 <CAS>

A;Cross-references: EMBL:X60864; NID:g52855; PIDN:CAA43254.1; PID:g52856

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 60.0%; Score 3; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 4 SRL 6

RESULT 6

S35627

uvrX protein - phage T6 (fragment)

C;Species: phage T6

C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 08-Oct-1999

C;Accession: S35627

R;Winkler, M.; Rueger, W.

Nucleic Acids Res. 21, 1500, 1993

A;Title: Cloning and sequencing of the genes of beta-glucosyl-HMC-alpha-glucosyl-transferase of bacteriophages T2 and T6.

A;Reference number: S35622; MUID:93219141; PMID:8464751

A;Accession: S35627

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-16 <WIN>

A;Cross-references: EMBL:X68725; NID:g296439; PIDN:CAA48668.1; PID:g296441

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992

Query Match 60.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 8 SRL 10

RESULT 7

A28587

T-cell receptor beta-2 chain J-B2.2 segment - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999

C;Accession: A28587

R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985

A;Title: Organization and sequences of the diversity, joining, and constant region genes of the human T-cell receptor beta chain.

A;Reference number: A94081; MUID:86094276; PMID:3866244

A;Accession: A28587

A;Molecule type: DNA

A;Residues: 1-16 <TOY>

A;Cross-references: GB:M14159; NID:g338852; PIDN:AAA60676.1; PID:g553687

C;Keywords: T-cell receptor

Query Match 60.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

Db           |||  
             11 SRL 13

RESULT 8

JP0068

ribosomal protein L30 - Thermomonospora curvata (fragment)

C;Species: Thermomonospora curvata

C;Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 28-Oct-1994

C;Accession: JP0068

R;Ochi, K.

submitted to JIPID, February 1994

A;Description: Phylogenetic diversity in the genus Bacillus and comparative  
ribosomal protein AT-L30 analyses of the genus Thermoactinomyces and relatives.

A;Reference number: JP0042

A;Accession: JP0068

A;Molecule type: protein

A;Residues: 1-17 <OCH>

C;Keywords: protein biosynthesis; ribosome

Query Match                   60.0%; Score 3; DB 2; Length 17;  
Best Local Similarity   100.0%; Pred. No. 9.6e+02;  
Matches       3; Conservative   0; Mismatches   0; Indels       0; Gaps       0;

Qy           2 SRL 4  
             |||  
Db           1 SRL 3

RESULT 9

E28587

T-cell receptor beta-2 chain J-B2.6 segment - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999

C;Accession: E28587

R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.

Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985

A;Title: Organization and sequences of the diversity, joining, and constant  
region genes of the human T-cell receptor beta chain.

A;Reference number: A94081; MUID:86094276; PMID:3866244

A;Accession: E28587

A;Molecule type: DNA

A;Residues: 1-17 <TOY>

A;Cross-references: GB:M14159; NID:g338852; PIDN:AAA60680.1; PID:g553691

C;Keywords: T-cell receptor

Query Match                   60.0%; Score 3; DB 2; Length 17;  
Best Local Similarity   100.0%; Pred. No. 9.6e+02;  
Matches       3; Conservative   0; Mismatches   0; Indels       0; Gaps       0;

QY           2 SRL 4  
             |||  
Db           12 SRL 14

RESULT 10

H53284

T-cell receptor beta 2 chain J region, Jbeta2.6 - rabbit  
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)  
 C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C;Accession: H53284  
 R;Harindranath, N.; Alexander, C.B.; Mage, R.G.  
 Mol. Immunol. 28, 881-888, 1991  
 A;Title: Evolutionarily conserved organization and sequences of germline diversity and joining regions of the rabbit T-cell receptor beta 2 chain.  
 A;Reference number: A53284; MUID:91342695; PMID:1678859  
 A;Accession: H53284  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-17 <HAR>  
 A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19524.1; PID:g233924  
 A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60746)  
 C;Keywords: T-cell receptor

Query Match 60.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 12 SRL 14

#### RESULT 11

PC1324

hypothetical protein 19 - curled-leaved tobacco chloroplast (fragment)  
 C;Species: chloroplast *Nicotiana plumbaginifolia* (curled-leaved tobacco)  
 C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 24-Feb-1995  
 C;Accession: PC1324  
 R;Fejes, E.; Engler, D.; Maliga, P.  
 Theor. Appl. Genet. 79, 28-32, 1990  
 A;Title: Extensive homologous chloroplast DNA recombination in the pt14 *Nicotiana* somatic hybrid.  
 A;Reference number: PC1321  
 A;Accession: PC1324  
 A;Molecule type: DNA  
 A;Residues: 1-19 <FEJ>  
 C;Genetics:  
 A;Genome: chloroplast  
 C;Keywords: chloroplast

Query Match 60.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 14 SRL 16

#### RESULT 12

PC1322

hypothetical protein 19 - common tobacco chloroplast (fragment)  
 C;Species: chloroplast *Nicotiana tabacum* (common tobacco)



C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 24-Feb-1995  
 C;Accession: PC1322  
 R;Fejes, E.; Engler, D.; Maliga, P.  
 Theor. Appl. Genet. 79, 28-32, 1990  
 A;Title: Extensive homologous chloroplast DNA recombination in the pt14  
 Nicotiana somatic hybrid.  
 A;Reference number: PC1321  
 A;Accession: PC1322  
 A;Molecule type: DNA  
 A;Residues: 1-19 <FEJ>  
 C;Genetics:  
 A;Genome: chloroplast  
 C;Keywords: chloroplast

Query Match 60.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
 |||  
 Db 14 SRL 16

#### RESULT 13

C20554

hemocyanin subunit IIa - Atlantic horseshoe crab (fragment)

C;Species: Limulus polyphemus (Atlantic horseshoe crab)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-May-1997

C;Accession: C20554

R;Lamy, J.; Lamy, J.; Sizaret, P.Y.; Billiald, P.; Jolles, P.; Jolles, J.;  
 Feldmann, R.J.; Bonaventura, J.

Biochemistry 22, 5573-5583, 1983

A;Title: Quaternary structure of Limulus polyphemus hemocyanin.

A;Reference number: A90478

A;Accession: C20554

A;Molecule type: protein

A;Residues: 1-20 <LAM>

C;Comment: Limulus polyphemus hemocyanin is an association of eight different  
 subunits within eight heterohexamers. Approximately 2 chains of subunit IIa are  
 found in the 48-mer.

C;Superfamily: hemocyanin

Query Match 60.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
 |||  
 Db 7 SRL 9

#### RESULT 14

I67551

monocyte chemotactic protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000

C;Accession: I67551

R;Steenbergen, E.J.; Verhagen, O.J.; van Leeuwen, E.F.; Behrendt, H.; Merle, P.A.; Wester, M.R.; von dem Borne, A.E.; van der Schoot, C.E.  
Eur. J. Immunol. 24, 900-908, 1994

A;Title: B precursor acute lymphoblastic leukemia third complementarity-determining regions predominantly represent an unbiased recombination repertoire: leukemic transformation frequently occurs in fetal life.

A;Reference number: I53401; MUID:94200227; PMID:8149961

A;Accession: I67551

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-20 <RES>

A;Cross-references: GB:S69743; NID:g546304; PIDN:AAD14041.1; PID:g4261741

C;Genetics:

A;Gene: IgH VDJ

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 16 SRL 18

#### RESULT 15

S35624

uvsX protein - phage T2 (fragment)

C;Species: phage T2

C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 08-Oct-1999

C;Accession: S35624

R;Winkler, M.; Rueger, W.

Nucleic Acids Res. 21, 1500, 1993

A;Title: Cloning and sequencing of the genes of beta-glucosyl-HMC-alpha-glucosyl-transferase of bacteriophages T2 and T6.

A;Reference number: S35622; MUID:93219141; PMID:8464751

A;Accession: S35624

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-22 <WIN>

A;Cross-references: EMBL:X68724; NID:g296435; PIDN:CAA48665.1; PID:g296438

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992

Query Match 60.0%; Score 3; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 8 SRL 10

#### RESULT 16

T14910

hypothetical protein - parsley

C;Species: Petroselinum crispum (parsley)

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000

C;Accession: T14910  
 R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.  
 Mol. Gen. Genet. 257, 595-605, 1998  
 A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of light dependent expression, post-transcriptional regulation, nuclear import and heterodimerisation.  
 A;Reference number: Z18261; MUID:98265918; PMID:9604882  
 A;Accession: T14910  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-5 <KIR>  
 A;Cross-references: EMBL:Y10810; NID:g3336904; PIDN:CAA71769.1; PID:g3336905  
 A;Experimental source: ssp. Hamburger Schnitt

Query Match 40.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 3 SR 4

#### RESULT 17

S53595  
 hypothetical protein (upstream of transcription factor, CCAAT-binding) - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
 C;Accession: S53595  
 R;Calkhoven, C.F.; Bouwman, P.R.J.; Snippe, L.; Ab, G.  
 Nucleic Acids Res. 22, 5540-5547, 1994  
 A;Title: Translation start site multiplicity of the CCAAT/enhancer binding protein alpha mRNA is dictated by a small 5' open reading frame.  
 A;Reference number: S53595; MUID:95140613; PMID:7838705  
 A;Accession: S53595  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-5 <CAL>  
 A;Cross-references: EMBL:X66844

Query Match 40.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 4 RL 5

#### RESULT 18

PT0525  
 T-cell receptor beta chain V-D-J region (100-4J) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PT0525  
 R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0525  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: adult thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 2 SR 3

#### RESULT 19

PT0577  
T-cell receptor beta chain V-D-J region (141-1BC) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0577; PT0574  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0577  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1BC  
A;Accession: PT0574  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FE2>  
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1Q  
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 3 SR 4

#### RESULT 20

PT0565  
T-cell receptor beta chain V-D-J region (141-1CF) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0565  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0565  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 3 SR 4

RESULT 21

PT0700  
T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0700  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0700  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 3 SR 4

RESULT 22

B33932  
Ig mu chain D region (D23) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 16-Aug-1996  
C;Accession: B33932  
R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989

A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-line genes.

A;Reference number: A33932; MUID:89282823; PMID:2499887

A;Accession: B33932

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-6 <BAC>

A;Cross-references: GB:M27107

C;Keywords: immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 4 RL 5

#### RESULT 23

PT0518

T-cell receptor beta chain V-D-J region (100-4B) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0518

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0518

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FEE>

A;Experimental source: adult thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 2 SR 3

#### RESULT 24

PT0662

T-cell receptor beta chain V-D-J region (121-3BA) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0662

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0662  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FEE>  
A;Experimental source: day 4 postnatal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 2 SR 3

RESULT 25

S19630  
ribosomal protein L30 - Streptomyces griseus (fragment)  
C;Species: Streptomyces griseus  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 06-Jun-1997  
C;Accession: S19630  
R;Ochi, K.  
Int. J. Syst. Bacteriol. 42, 144-150, 1992  
A;Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete genera.  
A;Reference number: S19630; MUID:92144363; PMID:1736962  
A;Accession: S19630  
A;Molecule type: protein  
A;Residues: 1-7 <OCH>  
A;Experimental source: strain IFO 13189  
C;Superfamily: Escherichia coli ribosomal protein L30  
C;Keywords: protein biosynthesis; ribosome

Query Match 40.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 2 RL 3

RESULT 26

ECMUCR  
catch-relaxing peptide - blue mussel  
N;Alternate names: CARP  
C;Species: Mytilus edulis (blue mussel)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: A29342  
R;Hirata, T.; Kubota, I.; Takabatake, I.; Kawahara, A.; Shimamoto, N.; Muneoka, Y.  
Brain Res. 422, 374-376, 1987  
A;Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.  
A;Reference number: A29342; MUID:88052022; PMID:3676797  
A;Accession: A29342  
A;Molecule type: protein

A;Residues: 1-7 <HIR>  
C;Comment: This peptide exhibits both potentiating (contraction) and inhibitory (relaxation) effects on the anterior byssus retractor muscle.  
C;Superfamily: unassigned animal peptides  
C;Keywords: amidated carboxyl end; hormone; retractor muscle  
F;7/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

#### RESULT 27

A15398  
choline oxidase (EC 1.1.3.17) - *Alcaligenes* sp. (tentative sequence) (fragment)  
C;Species: *Alcaligenes* sp.  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000  
C;Accession: A15398  
R;Ohta-Fukuyama, M.; Miyake, Y.; Emi, S.; Yamano, T.  
J. Biochem. 88, 197-203, 1980  
A;Title: Identification and properties of the prosthetic group of choline oxidase from *Alcaligenes* sp.  
A;Reference number: A15398; MUID:81006769; PMID:6997283  
A;Accession: A15398  
A;Molecule type: protein  
A;Residues: 1-7 <OHT>  
C;Keywords: oxidoreductase

Query Match 40.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 6 SR 7

#### RESULT 28

PN0150  
omega-gliadine 1' - *Aegilops longissima* (fragment)  
C;Species: *Aegilops longissima*  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: PN0150  
R;Odintsova, T.I.; Egorov, T.A.  
Biokhimiia 55, 509-516, 1990  
A;Title: N-Terminal sequences of omega-gliadins of *Aegilops longissima*: On the origin of polyploid wheat genomes.  
A;Reference number: PN0146; MUID:90283493; PMID:2354218  
A;Accession: PN0150  
A;Molecule type: protein  
A;Residues: 1-7 <ODI>  
A;Experimental source: strain K-907



Query Match 40.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 1 SR 2

RESULT 29

A28340

myomodulin - California sea hare

C;Species: Aplysia californica (California sea hare)

C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 18-Jun-1993

C;Accession: A28340

R;Cropper, E.C.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5483-5486, 1987

A;Title: Myomodulin: A bioactive neuropeptide present in an identified  
cholinergic buccal motor neuron of Aplysia.

A;Reference number: A28340; MUID:87261010; PMID:3474664

A;Accession: A28340

A;Molecule type: protein

A;Residues: 1-7 <CRO>

Query Match 40.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

RESULT 30

PT0671

T-cell receptor beta chain V-D-J region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 04-Mar-2000

C;Accession: PT0671; PT0564; PT0537; PT0536; PT0682

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N  
regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0671

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-7 <FEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 140-1K

A;Accession: PT0564

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FE1>

A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1CE

A;Accession: PT0537

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FE2>  
A;Experimental source: adult thymus, strain BALB/c, clone 126-1CH  
A;Accession: PT0536  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FE3>  
A;Experimental source: adult thymus, strain BALB/c, clone 126-1CC  
A;Accession: PT0682  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-3 <FE4>  
A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 140-1B  
C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 2 SR 3

RESULT 31

PH0932

T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0932

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental  
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0932

A;Molecule type: mRNA

A;Residues: 1-7 <GOL>

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

RESULT 32

LFSAME

probable msrA leader peptide - Staphylococcus epidermidis

C;Species: Staphylococcus epidermidis

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Jul-1999

C;Accession: S11157

R;Ross, J.I.; Eady, E.A.; Cove, J.H.; Cunliffe, W.J.; Baumberg, S.; Wootton,  
J.C.

Mol. Microbiol. 4, 1207-1214, 1990

A;Title: Inducible erythromycin resistance in staphylococci is encoded by a member of the ATP-binding transport super-gene family.

A;Reference number: S11157; MUID:91041730; PMID:2233255

A;Accession: S11157

A;Molecule type: DNA

A;Residues: 1-8 <ROS>

A;Cross-references: EMBL:X52085; NID:g47000; PIDN:CAA36303.1; PID:g581653

C;Superfamily: probable msrA leader peptide

Query Match 40.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
||  
Db 6 RL 7

### RESULT 33

PH1407

Ig heavy chain V region (clone micro m+ 46-6 PCR) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999

C;Accession: PH1407

R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Takemori, T.

J. Exp. Med. 176, 1209-1214, 1992

A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in the progeny of a single precursor cell transformed with a temperature-sensitive mutant of abelson murine leukemia virus.

A;Reference number: PH1403; MUID:93018837; PMID:1402663

A;Accession: PH1407

A;Molecule type: DNA

A;Residues: 1-8 <SHI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
||  
Db 4 RL 5

### RESULT 34

T10077

hypothetical protein N - Methylophilus methylotrophus (fragment)

C;Species: Methylophilus methylotrophus

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000

C;Accession: T10077

R;Chistoserdov, A.Y.; McIntire, W.S.; Mathews, F.S.; Lidstrom, M.E.

J. Bacteriol. 176, 4073-4080, 1994

A;Title: Organization of the methylamine utilization (mau) genes in Methylophilus methylotrophus W3A1-NS.

A;Reference number: Z16936; MUID:94292427; PMID:8021188  
A;Accession: T10077  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-8 <CHI>  
A;Cross-references: EMBL:L26407; NID:g561931; PIDN:AAB46955.1; PID:g561933  
A;Experimental source: strain W3A1  
C;Genetics:  
A;Gene: mauN

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 3 RL 4

#### RESULT 35

PC4131

hypothetical protein 8 [imported] - *Pseudomonas aeruginosa* (fragment)

C;Species: *Pseudomonas aeruginosa*

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000

C;Accession: PC4131

R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.

Gene 167, 87-91, 1995

A;Title: Sequencing and characterization of the downstream region of the genes encoding nitrite reductase and cytochrome c-551 (nirSM) from *Pseudomonas aeruginosa*: Identification of the gene necessary for biosynthesis of heme d1.

A;Reference number: JC4552; MUID:96144254; PMID:8566817

A;Accession: PC4131

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-8 <KAW>

A;Cross-references: DDBJ:D50473; NID:g1217594

A;Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 5 SR 6

#### RESULT 36

PL0162

paramyosin - northern quahog (fragment)

C;Species: *Mercenaria mercenaria* (northern quahog)

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 11-May-2000

C;Accession: PL0162

R;Watabe, S.; Tsuchiya, T.; Hartshorne, D.J.

Comp. Biochem. Physiol. B 94, 813-821, 1989

A;Title: Phosphorylation of paramyosin.

A;Reference number: PL0162; MUID:90107385; PMID:2532591

A;Accession: PL0162  
 A;Molecule type: protein  
 A;Residues: 1-8 <WAT>  
 A;Experimental source: white adductor muscle  
 A;Note: the sequence is the phosphorylated tryptic peptide  
 C;Comment: This protein is thought to exist as a dimer of two subunits, termed alpha-paramyosin. Alpha-paramyosin is degraded by proteolysis to beta-paramyosin which involves the loss of a segment from the carboxyl-terminal end of the molecule. Only alpha-paramyosin is phosphorylated by an endogenous kinase.  
 C;Keywords: muscle; phosphoprotein  
 F;5/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 1 SR 2

#### RESULT 37

A23967

leucopyrokinin - Madeira cockroach

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 31-Mar-1988 #sequence\_revision 26-May-1994 #text\_change 11-Jul-1997

C;Accession: A23967

R;Nachman, R.J.; Holman, G.M.; Cook, B.J.

Biochem. Biophys. Res. Commun. 137, 936-942, 1986

A;Title: Active fragments and analogs of the insect neuropeptide leucopyrokinin: structure-function studies.

A;Reference number: A23967; MUID:86269041; PMID:3015140

A;Accession: A23967

A;Molecule type: protein

A;Residues: 1-8 <NAC>

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 7 RL 8

#### RESULT 38

T13818

cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)

C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000

C;Accession: T13818

R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.

Mol. Biol. Evol. 14, 807-813, 1997

A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI genes were established in the common ancestor with the lancelet.  
A;Reference number: Z17775; MUID:97398704; PMID:9254918  
A;Accession: T13818  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-8 <DEL>  
A;Cross-references: EMBL:Y09527; NID:g2340019; PIDN:CAA70718.1; PID:g2340022  
C;Genetics:  
A;Genome: mitochondrion  
A;Note: COI  
C;Keywords: mitochondrion

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 4 SR 5

RESULT 39

A59028

MHC class I histocompatibility antigen HLA-C alpha chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-2001 #sequence\_revision 31-Dec-2001 #text\_change 31-Dec-2001

C;Accession: A59028

R;Escolano, J.M.

submitted to the Protein Sequence Database, August 1998

A;Reference number: A59028

A;Accession: A59028

A;Molecule type: protein

A;Residues: 1-8 <ESC>

C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen

Query Match 40.0%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 7 SR 8

RESULT 40

B45796

dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) - Pseudomonas fluorescens (fragment)

C;Species: Pseudomonas fluorescens

C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 05-May-2000

C;Accession: B45796

R;Benen, J.A.E.; Van Berkel, W.J.H.; Van Dongen, W.M.A.M.; Mueller, F.; De Kok, A.

J. Gen. Microbiol. 135, 1787-1797, 1989

A;Title: Molecular cloning and sequence determination of the lpd gene encoding lipoamide dehydrogenase from *Pseudomonas fluorescens*.  
A;Reference number: A45796; MUID:90132584; PMID:2515251  
A;Accession: B45796  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-9 <BEN>  
A;Cross-references: GB:M28356; NID:g151343; PIDN:AAA99233.1; PID:g151344  
C;Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology  
C;Keywords: acyltransferase; coenzyme A; lipoamide; tricarboxylic acid cycle

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 4 RL 5

#### RESULT 41

A61620

locustamyotropin III - migratory locust

C;Species: *Locusta migratoria* (migratory locust)

C;Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 11-Jul-1997

C;Accession: A61620

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.

Insect Biochem. Mol. Biol. 22, 447-452, 1992

A;Title: Isolation, identification and synthesis of locustamyotropin III and IV, two additional neuropeptides of *Locusta migratoria*: members of the locustamyotropin peptide family.

A;Reference number: A61620

A;Accession: A61620

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-9 <SCH>

C;Keywords: amidated carboxyl end; neuropeptide

F;9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 8 RL 9

#### RESULT 42

S78762

ribosomal protein MRP-S12, mitochondrial - bovine (fragment)

C;Species: *Bos primigenius taurus* (cattle)

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C;Accession: S78762

R;Graack, H.R.

submitted to the Protein Sequence Database, July 1999  
A;Reference number: S78760  
A;Accession: S78762  
A;Molecule type: protein  
A;Residues: 1-9 <GRA>  
C;Keywords: mitochondrion  
F;1-9/Product: ribosomal protein MRP-S12 (fragment) #status experimental <MAT>

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 8 RL 9

#### RESULT 43

S78420  
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000  
C;Accession: S78420  
R;Goldschmidt-Reisin, S.; Graack, H.R.  
submitted to the Protein Sequence Database, February 1998  
A;Reference number: S78411  
A;Accession: S78420  
A;Molecule type: protein  
A;Residues: 1-9 <GOL>  
A;Note: the protein is designated as mitochondrial ribosomal protein L41  
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 40.0%; Score 2; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

#### RESULT 44

B33710  
ornithine decarboxylase leader peptide - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 27-Feb-1990 #sequence\_revision 27-Feb-1990 #text\_change 24-Sep-1999  
C;Accession: B33710  
R;Wen, L.; Huang, J.K.; Blackshear, P.J.  
J. Biol. Chem. 264, 9016-9021, 1989  
A;Title: Rat ornithine decarboxylase gene. Nucleotide sequence, potential regulatory elements, and comparison to the mouse gene.  
A;Reference number: A33710; MUID:89255378; PMID:2722815  
A;Accession: B33710  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-10 <WEN>



A;Cross-references: GB:J04791; NID:g205807; PIDN:AAA66163.1; PID:g806309  
C;Superfamily: unassigned leader peptides

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 5 SR 6

RESULT 45

C39191

hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis

C;Species: Bacteroides fragilis

C;Date: 08-Nov-1991 #sequence\_revision 08-Nov-1991 #text\_change 30-Sep-1993

C;Accession: C39191

R;Speer, B.S.; Bedzyk, L.; Salyers, A.A.

J. Bacteriol. 173, 176-183, 1991

A;Title: Evidence that a novel tetracycline resistance gene found on two  
Bacteroides transposons encodes an NADP-requiring oxidoreductase.

A;Reference number: A39191; MUID:91100280; PMID:1846135

A;Accession: C39191

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-10 <SPE>

A;Cross-references: GB:M37699

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 4 SR 5

RESULT 46

PC2044

beta-Kirilowin - Mongolian snake-gourd (fragment)

C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)

C;Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 17-Mar-1999

C;Accession: PC2044

R;Dong, T.X.; Ng, T.B.; Yeung, H.W.; Wong, R.N.S.

Biochem. Biophys. Res. Commun. 199, 387-393, 1994

A;Title: Isolation and characterization of a novel ribosome-inactivating  
protein, beta-kirilowin, from the seeds of Trichosanthes kirilowii.

A;Reference number: PC2044; MUID:94168605; PMID:8123040

A;Accession: PC2044

A;Molecule type: protein

A;Residues: 1-10 <DON>

A;Experimental source: seed

C;Comment: This protein exhibited strong abortifacient activity, and is a  
ribosome inactivating protein.

C;Keywords: seed

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

RESULT 47

S19296

16K protein - poulard wheat

C;Species: Triticum turgidum (poulard wheat)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C;Accession: S19296

R;Sanchez-Monge, R.; Gomez, L.; Barber, D.; Lopez-Otin, C.; Armentia, A.;  
Salcedo, G.

Biochem. J. 281, 401-405, 1992

A;Title: Wheat and barley allergens associated with baker's asthma. Glycosylated  
subunits of the alpha-amylase-inhibitor family have enhanced IgE-binding  
capacity.

A;Reference number: S19296; MUID:92143804; PMID:1736890

A;Accession: S19296

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SAN>

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 1 SR 2

RESULT 48

PT0309

Ig heavy chain CRD3 region (clone 6-94) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0309

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain  
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0309

A;Molecule type: DNA

A;Residues: 1-10 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SR 3  
||  
Db 6 SR 7

RESULT 49

PT0212

T-cell receptor alpha chain V-J region (4-1-E.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C;Accession: PT0212

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0212

A;Molecule type: mRNA

A;Residues: 1-10 <NAK>

C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
||  
Db 9 RL 10

RESULT 50

PH0894

T-cell receptor beta chain V-D-J region (clone 5) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997

C;Accession: PH0894

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0894

A;Molecule type: mRNA

A;Residues: 1-10 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
||  
Db 9 RL 10

Search completed: November 28, 2003, 14:32:38

Job time : 23 secs

OM protein - protein search, using sw model

Run on: November 28, 2003, 14:26:13 ; Search time 11 Seconds  
 (without alignments)  
 21.376 Million cell updates/sec

Title: US-09-228-866-45  
 Perfect score: 5  
 Sequence: 1 XSRLX 5

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1411

Minimum DB seq length: 5  
 Maximum DB seq length: 23

Post-processing: Listing first 100 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score					
1	3	60.0	12	1	YZPY_ECOLI	P17776 escherichia
2	3	60.0	16	1	UVSX_BPT6	Q06728 bacterioph
3	3	60.0	22	1	UVSX_BPT2	Q06727 bacterioph
4	2	40.0	7	1	CARP_MYTED	P10420 mytilus edu
5	2	40.0	7	1	CHOX_ALCSP	P16101 alcaligenes
6	2	40.0	8	1	ALL3_CYDPO	P82154 cydia pomon
7	2	40.0	8	1	FAR4_MACRS	P83277 macrobrachi
8	2	40.0	8	1	LMT2_LOCFI	P22396 locusta mig
9	2	40.0	8	1	LPK_LEUMA	P13049 leucophaea
10	2	40.0	8	1	LPMS_STAEP	P23211 staphylococ
11	2	40.0	8	1	PPK2_PERAM	P82692 periplaneta
12	2	40.0	8	1	PPK3_PERAM	P82618 periplaneta
13	2	40.0	9	1	FAR3_PENMO	P83318 penaeus mon
14	2	40.0	9	1	FAR4_PENMO	P83319 penaeus mon
15	2	40.0	9	1	FAR5_PENMO	P83320 penaeus mon
16	2	40.0	9	1	LMT3_LOCFI	P41489 locusta mig
17	2	40.0	9	1	PPK1_PERAM	P82691 periplaneta

18	2	40.0	10	1	AKHX_LOCFMI	P81626	locusta mig
19	2	40.0	10	1	FAR5_MACRS	P83278	macrobrachi
20	2	40.0	10	1	GS09_BACSU	P80243	bacillus su
21	2	40.0	10	1	LPK2_LOCFMI	P41488	locusta mig
22	2	40.0	10	1	MALE_KLEPN	Q05564	klebsiella
23	2	40.0	10	1	RT02_BOVIN	P82923	bos taurus
24	2	40.0	10	1	TKU1_UREUN	P40751	urechis uni
25	2	40.0	11	1	CORZ_PERAM	P11496	periplaneta
26	2	40.0	11	1	FAR6_PENMO	P83321	penaeus mon
27	2	40.0	11	1	PKC1_CARMO	P82684	carausius m
28	2	40.0	12	1	LMT1_LOCFMI	P22395	locusta mig
29	2	40.0	12	1	PPK4_PERAM	P82619	periplaneta
30	2	40.0	12	1	PPK4_PERFU	P82690	periplaneta
31	2	40.0	12	1	RR16_GINBI	P36207	ginkgo bilo
32	2	40.0	13	1	LMT4_LOCFMI	P41490	locusta mig
33	2	40.0	13	1	NEUT_CAVPO	P32560	cavia porce
34	2	40.0	14	1	ALYT_ALYOB	P08944	alytes obst
35	2	40.0	14	1	KLPS_SCARA	P58396	scaptocosa
36	2	40.0	14	1	LPER_BACLI	Q04303	bacillus li
37	2	40.0	14	1	PPK6_PERAM	P82693	periplaneta
38	2	40.0	14	1	SAP2_ARBPU	P11760	arbacia pun
39	2	40.0	15	1	CX3B_CONQU	P58842	conus querc
40	2	40.0	15	1	RS10_BACST	P59683	bacillus st
41	2	40.0	15	1	TA1_TREBR	P34070	tremella br
42	2	40.0	15	1	UC13_MAIZE	P80619	zea mays (m
43	2	40.0	15	1	UC25_MAIZE	P80631	zea mays (m
44	2	40.0	15	1	URE1_MORMO	P17337	morganella
45	2	40.0	16	1	AF2S_MALPA	P83142	malva parvi
46	2	40.0	16	1	FOR1_MYRGU	P81438	myrmecia gu
47	2	40.0	16	1	FOR2_MYRGU	P81437	myrmecia gu
48	2	40.0	16	1	LPK1_LOCFMI	P20404	locusta mig
49	2	40.0	16	1	PGTL_PELAC	P80563	pelobacter
50	2	40.0	16	1	YMOR_PSEPU	Q02210	pseudomonas
51	2	40.0	17	1	APID_BOMPA	P81464	bombus pasc
52	2	40.0	17	1	PA2_AUSSU	P59066	austrelaps
53	2	40.0	17	1	PC24_BRANA	P81097	brassica na
54	2	40.0	17	1	PPK5_PERAM	P82617	periplaneta
55	2	40.0	17	1	RM35_YEAST	P36530	saccharomyc
56	2	40.0	17	1	SP51_BACLI	P27642	bacillus li
57	2	40.0	18	1	ALL2_CYDPO	P82153	cydia pomon
58	2	40.0	18	1	GOME_ACAGO	P82358	acanthoscur
59	2	40.0	18	1	PHPT_PSESE	P25271	pseudaletia
60	2	40.0	18	1	YAA5_RHOPA	Q02005	rhodopseudo
61	2	40.0	19	1	FIBB_LAMGL	P14473	lama glama
62	2	40.0	19	1	HI70_RAT	P21794	rattus norv
63	2	40.0	19	1	UKA1_HUMAN	P31940	homo sapien
64	2	40.0	20	1	AROQ_AMEYE	P46380	amycolatops
65	2	40.0	20	1	CLPB_ACICA	P82956	acinetobact
66	2	40.0	20	1	FLAW_AZOVI	P52964	azotobacter
67	2	40.0	20	1	FRHA_METBA	P80489	methanosarc
68	2	40.0	20	1	PL2_LUPLU	P83364	lupinus lut
69	2	40.0	20	1	PL4_LUPLU	P83366	lupinus lut
70	2	40.0	20	1	UCRQ_EQUAR	P81247	equisetum a
71	2	40.0	20	1	VMO2_CHICK	Q9ps49	gallus gall
72	2	40.0	21	1	FA71_TETPY	P81424	tetrahymena
73	2	40.0	21	1	FIBB_ANTAM	P14465	antilocapra
74	2	40.0	21	1	LPRM_CORDI	P21232	corynebacte

75	2	40.0	21	1	MCT3_MOUSE	P21843	mus musculu
76	2	40.0	21	1	OMPI_HAEPR	P80369	haemophilus
77	2	40.0	21	1	REV_HV2D2	P15830	human immun
78	2	40.0	22	1	ANFC_CHICK	P21805	gallus gall
79	2	40.0	22	1	CO4_CAVPO	P19069	cavia porce
80	2	40.0	22	1	CPI4_SOLTU	P58602	solanum tub
81	2	40.0	22	1	KORB_METTM	P80905	methanobact
82	2	40.0	22	1	LPL_CORGL	P42456	corynebacte
83	2	40.0	22	1	RL41_METJA	P54025	methanococc
84	2	40.0	23	1	ALL5_HORSE	P82616	equus cabal
85	2	40.0	23	1	BR1B_RANES	P40836	rana escule
86	2	40.0	23	1	GLNA_PHOLP	P20479	phormidium
87	2	40.0	23	1	IAPP_LEPEU	Q07333	lepus europ
88	2	40.0	23	1	PQQA_KLEPN	P27503	klebsiella
89	2	40.0	23	1	T2A_PARTE	Q27173	paramecium
90	2	40.0	23	1	T2B_PARTE	Q27174	paramecium
91	2	40.0	23	1	TL17_SPIOL	P81778	spinacia ol
92	2	40.0	23	1	TYPH_LACRH	P19663	lactobacill
93	2	40.0	23	1	UDP_LACRH	P19662	lactobacill
94	1	20.0	5	1	AL14_CARMA	P81817	carcinus ma
95	1	20.0	5	1	BIOB_CITFR	P12997	citrobacter
96	1	20.0	5	1	FARP_ARTTR	P41853	artioposthi
97	1	20.0	5	1	PRCT_PERAM	P01373	periplaneta
98	1	20.0	5	1	UF01_MOUSE	P38639	mus musculu
99	1	20.0	5	1	UXA4_CHLTR	P38005	chlamydia t
100	1	20.0	6	1	ACPH_RABIT	P25154	oryctolagus

# ALIGNMENTS

## RESULT 1

### YZPY\_ECOLI

ID YZPY\_ECOLI STANDARD; PRT; 12 AA.  
AC P17776;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 01-AUG-1992 (Rel. 23, Last annotation update)  
DE Hypothetical pyrE leader peptide.  
GN PYRL OR PYRE-LP.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85003588; PubMed=6207018;  
RA Poulsen P., Bonekamp F., Jensen K.F.;  
RT "Structure of the Escherichia coli pyrE operon and control of pyrE  
RT expression by a UTP modulated intercistronic attentuation.";  
RL EMBO J. 3:1783-1790(1984).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=83287414; PubMed=6349999;  
RA Poulsen P., Jensen K.F., Valentin-Hansen P., Carlsson P.,  
RA Lundberg L.G.;

RT "Nucleotide sequence of the Escherichia coli pyrE gene and of the DNA  
 RT in front of the protein-coding region.";  
 RL Eur. J. Biochem. 135:223-229(1983).  
 CC -!- CAUTION: THIS SEQUENCE, ACCORDING TO THE ECOSEQ DATABASE (K. RUDD)  
 CC IS PROBABLY NOT A REAL PROTEIN; THEREFORE THIS ENTRY WILL PROBABLY  
 CC BE DELETED IN FUTURE RELEASES.  
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 CC -----  
 DR EMBL; X00781; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL; V01578; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A30400; LFECPE.  
 KW Hypothetical protein.  
 SQ SEQUENCE 12 AA; 1542 MW; C4291FA437A2C9C9 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
 |||  
 Db 2 SRL 4

## RESULT 2

### UVSX\_BPT6

ID UVSX\_BPT6 STANDARD; PRT; 16 AA.  
 AC Q06728;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Recombination and repair protein (Fragment).  
 GN UVSX.  
 OS Bacteriophage T6.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 OC T4-like viruses.  
 OX NCBI\_TaxID=10666;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93219141; PubMed=8464751;  
 RA Winkler M., Rueger W.;  
 RT "Cloning and sequencing of the genes of  
 RT beta-glucosyl-HMC-alpha-glucosyl-transferases of bacteriophages T2  
 RT and T6.";  
 RL Nucleic Acids Res. 21:1500-1500(1993).  
 CC -!- FUNCTION: IMPORTANT IN GENETIC RECOMBINATION, DNA REPAIR, AND  
 CC REPLICATION. POSSESSES PAIRING AND STRAND-TRANSFER ACTIVITY.  
 CC INTERACTS WITH DDA AND GENE 32 PROTEINS.  
 CC -!- SIMILARITY: Belongs to the recA family.  
 CC -----  
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DR EMBL; X68725; CAA48668.1; -.  
DR PIR; S35627; S35627.  
KW DNA damage; DNA replication; DNA recombination; DNA repair;  
KW ATP-binding.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1721 MW; 48164C95D76F3CB4 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 8 SRL 10

### RESULT 3

#### UVSX\_BPT2

ID UVSX\_BPT2 STANDARD; PRT; 22 AA.  
AC Q06727;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Recombination and repair protein (Fragment).  
GN UVSX.  
OS Bacteriophage T2.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
OC T4-like viruses.  
OX NCBI\_TaxID=10664;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93219141; PubMed=8464751;  
RA Winkler M., Rueger W.;  
RT "Cloning and sequencing of the genes of  
RT beta-glucosyl-HMC-alpha-glucosyl-transferases of bacteriophages T2  
RT and T6.";  
RL Nucleic Acids Res. 21:1500-1500(1993).  
CC -!- FUNCTION: IMPORTANT IN GENETIC RECOMBINATION, DNA REPAIR, AND  
CC REPLICATION. POSSESSES PAIRING AND STRAND-TRANSFER ACTIVITY.  
CC INTERACTS WITH DDA AND GENE 32 PROTEINS.  
CC -!- SIMILARITY: Belongs to the reca family.  
CC -----

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DR EMBL; X68724; CAA48665.1; -.  
 DR PIR; S35624; S35624.  
 KW DNA damage; DNA replication; DNA recombination; DNA repair;  
 KW ATP-binding.  
 FT NON\_TER 22 22  
 SQ SEQUENCE 22 AA; 2395 MW; 00AFC6821020D816 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
 |||  
 Db 8 SRL 10

#### RESULT 4

##### CARP\_MYTED

ID CARP\_MYTED STANDARD; PRT; 7 AA.  
 AC P10420;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last annotation update)  
 DE Catch-relaxing peptide (CARP).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=88052022; PubMed=3676797;  
 RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,  
 RA Muneoka Y.;  
 RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";  
 RL Brain Res. 422:374-376(1987).  
 CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)  
 CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS  
 CC RETRACTOR MUSCLE.  
 DR PIR; A29342; ECMUCR.  
 KW Hormone; Amidation.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
 ||  
 Db 6 RL 7

#### RESULT 5

##### CHOX\_ALCSP

ID CHOX\_ALCSP STANDARD; PRT; 7 AA.  
 AC P16101;  
 DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DE Choline oxidase (EC 1.1.3.17) (Fragment).  
 OS Alcaligenes sp.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Alcaligenaceae; Alcaligenes.  
 OX NCBI\_TaxID=512;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=81006769; PubMed=6997283;  
 RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;  
 RT "Identification and properties of the prosthetic group of choline  
 RT oxidase from Alcaligenes sp.";  
 RL J. Biochem. 88:197-203(1980).  
 CC -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).  
 DR PIR; A15398; A15398.  
 KW Oxidoreductase.  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SR 3  
 ||  
 Db 6 SR 7

#### RESULT 6

##### ALL3\_CYDPO

ID ALL3\_CYDPO STANDARD; PRT; 8 AA.  
 AC P82154;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 3.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily";  
 RL Peptides 18:1301-1309(1997).  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 926 MW; C82879D5AB477415 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 1 SR 2

#### RESULT 7

##### FAR4\_MACRS

ID FAR4\_MACRS STANDARD; PRT; 8 AA.  
AC P83277;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP4 (APALRLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
OX NCBI\_TaxID=79674;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RA Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,  
RA Sithigorngul W.;  
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
RT freshwater prawn Macrobrachium rosenbergii.";  
RL Comp. Biochem. Physiol. 120B:587-595(1998).  
CC -!- MASS SPECTROMETRY: MW=943; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 943 MW; 9CD40734072DC76D CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 5 RL 6

#### RESULT 8

##### LMT2\_LOCFI

ID LMT2\_LOCFI STANDARD; PRT; 8 AA.  
AC P22396;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-AUG-1991 (Rel. 19, Last annotation update)  
DE Locustamyotropin 2 (LOM-MT-2).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
 RT "Isolation, identification and synthesis of locustamyotropin II, an  
 RT additional neuropeptide of Locusta migratoria. Member of the  
 RT cephalomyotropic peptide family.";  
 RL Insect Biochem. 20:479-484(1990).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 934 MW; 26341771A9CAA87B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 7 RL 8

#### RESULT 9

##### LPK\_LEUMA

ID LPK\_LEUMA STANDARD; PRT; 8 AA.  
 AC P13049;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leukopyrokinin (LPK) (LEM-PK).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=86269041; PubMed=3015140;  
 RA Nachman R.J., Holman G.M., Cook B.J.;  
 RT "Active fragments and analogs of the insect neuropeptide  
 RT leucopyrokinin: structure-function studies.";  
 RL Biochem. Biophys. Res. Commun. 137:936-942(1986).  
 RN [2]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Head;  
 RX MEDLINE=87052651; PubMed=2877794;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Primary structure and synthesis of a blocked myotropic  
 RT neuropeptide isolated from the cockroach, Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 85C:219-224(1986).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).

CC -!- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS  
 CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE  
 CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPK MOST  
 CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE  
 CC PENTAPEPTIDE FRAGMENT FTPRL.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR PIR; A23967; A23967.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 949 MW; 92341771A9D5A1B6 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
 ||  
 Db 7 RL 8

# RESULT 10

## LPMS\_STAEP

ID LPMS\_STAEP STANDARD; PRT; 8 AA.  
 AC P23211;  
 DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE Probable msrA leader peptide.  
 OS Staphylococcus epidermidis.  
 OG Plasmid pUL5050.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1282;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=968;  
 RX MEDLINE=91041730; PubMed=2233255;  
 RA Ross J.I., Eady E.A., Cove J.H., Cunliffe W.J., Baumberg S.,  
 RA Wootton J.C.;  
 RT "Inducible erythromycin resistance in staphylococci is encoded by a  
 RT member of the ATP-binding transport super-gene family."  
 RL Mol. Microbiol. 4:1207-1214(1990).  
 CC -!- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE  
 CC PROTEIN.

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 CC -----  
 DR EMBL; X52085; CAA36303.1; -.  
 DR PIR; S11157; LFSAME.

KW Leader peptide; Plasmid.  
SQ SEQUENCE 8 AA; 937 MW; FA37340685BDC1A6 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

RESULT 11

PPK2\_PERAM

ID PPK2\_PERAM STANDARD; PRT; 8 AA.  
AC P82692;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=97353923; PubMed=9210163;  
RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;  
RT "Isolation and structural elucidation of two pyrokinins from the  
retrocerebral complex of the American cockroach.";  
RL Peptides 18:473-478(1997).  
RN [2]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
(MYOTROPIC ACTIVITY).  
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||

Db

7 RL 8

RESULT 12

PPK3\_PERAM

ID PPK3\_PERAM STANDARD; PRT; 8 AA.  
AC P82618;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Retrocerebral complex;  
RX MEDLINE=99212469; PubMed=10196736;  
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
RT "Differential distribution of pyrokinin-isoforms in cerebral and  
RT abdominal neurohemal organs of the American cockroach.";  
RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
RN [2]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
RT the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -!- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4

||

Db 7 RL 8

RESULT 13

FAR3\_PENMO

ID FAR3\_PENMO STANDARD; PRT; 9 AA.  
AC P83318;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP3 (AQPSMRLRF-amide).

OS *Penaeus monodon* (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; *Penaeus*.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn *Penaeus monodon*.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 6 RL 7

#### RESULT 14

##### FAR4\_PENMO

ID FAR4\_PENMO STANDARD; PRT; 9 AA.  
 AC P83319;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP4 (SQPSMRLRF-amide).  
 OS *Penaeus monodon* (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; *Penaeus*.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn *Penaeus monodon*.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.



KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
||  
Db 6 RL 7

RESULT 15

FAR5\_PENMO

ID FAR5\_PENMO STANDARD; PRT; 9 AA.  
AC P83320;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP5 (SMPSLRLRF-amide).  
OS Penaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
RT of the giant tiger prawn Penaeus monodon.";  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
||  
Db 6 RL 7

RESULT 16

LMT3\_LOCFMI

ID LMT3\_LOCFMI STANDARD; PRT; 9 AA.  
AC P41489;  
DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Locustamyotropin 3 (LOM-MT-3).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Brain;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,  
 RA de Loof A.;  
 RT "Isolation, identification and synthesis of locustamyotropin III and  
 RT IV, two additional neuropeptides of Locusta migratoria: members of the  
 RT locustamyotropin peptide family.";  
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).  
 CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR PIR; A61620; A61620.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
 ||  
 Db 8 RL 9

#### RESULT 17

##### PPK1\_PERAM

ID PPK1\_PERAM STANDARD; PRT; 9 AA.  
 AC P82691;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-1 (Pea-PK-1) (FXPRL-amide).  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=97353923; PubMed=9210163;  
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of two pyrokinins from the  
 RT retrocerebral complex of the American cockroach.";  
 RL Peptides 18:473-478(1997).

RN [2]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
 RT the American cockroach.";   
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
 CC -!- MASS SPECTROMETRY: MW=1010.4; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1011 MW; 885C176059C87DC1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
 ||  
 Db 8 RL 9

# RESULT 18

AKHX\_LOCFI

ID AKHX\_LOCFI STANDARD; PRT; 10 AA.  
 AC P81626;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Peptide hormone.  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RA Siebert K.J.;  
 RL Submitted (DEC-1998) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: PROBABLY INVOLVED IN THE REGULATION OF LOCUST  
 CC INTERMEDIARY METABOLISM, BEHAVIOR AND/OR DEVELOPMENT.  
 CC -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.  
 DR InterPro; IPR002047; AKH.  
 DR PROSITE; PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 5 SR 6

RESULT 19

FAR5\_MACRS

ID FAR5\_MACRS STANDARD; PRT; 10 AA.  
AC P83278;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP5 (DRTPALRLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
OX NCBI\_TaxID=79674;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RA Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,  
RA Sithigorngul W.;  
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
RT freshwater prawn Macrobrachium rosenbergii.";  
RL Comp. Biochem. Physiol. 120B:587-595(1998).  
CC -!- MASS SPECTROMETRY: MW=1243.4; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1244 MW; 9A1A5334072DC771 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 7 RL 8

RESULT 20

GS09\_BACSU

ID GS09\_BACSU STANDARD; PRT; 10 AA.  
AC P80243;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE General stress protein 9 (GSP9) (Fragment).  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]

RP SEQUENCE.  
 RC STRAIN=168 / IS58;  
 RX MEDLINE=94282319; PubMed=8012595;  
 RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,  
 RA Schmid R., Mach H., Hecker M.;  
 RT "Analysis of the induction of general stress proteins of *Bacillus*  
 RT *subtilis*.";   
 RL Microbiology 140:741-752(1994).  
 CC -!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE  
 CC LIMITATION AND OXYGEN LIMITATION.  
 CC -!- CAUTION: Could not be found in the genome of *B.subtilis* 168.  
 KW Heat shock.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1168 MW; 99766442D5A2C05A CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 1 SR 2

# RESULT 21

LPK2\_LOCFMI  
 ID LPK2\_LOCFMI STANDARD; PRT; 10 AA.  
 AC P41488;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=94094539; PubMed=7903606;  
 RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,  
 RA de Loof A.;  
 RT "Isolation, identification and synthesis of locustapyrokinin II from  
 RT *Locusta migratoria*, another member of the FXPRL-amide peptide  
 RT family.";   
 RL Comp. Biochem. Physiol. 106C:103-109(1993).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC  
 CC ACTIVITY).  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
||  
Db 9 RL 10

RESULT 22

MALE\_KLEPN

ID MALE\_KLEPN STANDARD; PRT; 10 AA.  
AC Q05564;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Maltose-binding periplasmic protein (Maltodextrin-binding protein)  
DE (MMBP) (Fragment).  
GN MALE.  
OS Klebsiella pneumoniae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1033-5P14 / KAY2026;  
RX MEDLINE=93211295; PubMed=8459773;  
RA Bachellier S., Perrin D., Hofnung M., Gilson E.;  
RT "Bacterial interspersed mosaic elements (BIMEs) are present in the  
RT genome of Klebsiella.";  
RL Mol. Microbiol. 7:537-544(1993).  
CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE  
CC TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND  
CC CHEMOTAXIS TOWARD MALTOOLIGOSACCHARIDES.  
CC -!- SUBCELLULAR LOCATION: Periplasmic.  
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING  
CC PROTEIN FAMILY 1.  
CC -----  
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CC -----  
DR EMBL; X68329; CAA48406.1; -.  
DR InterPro; IPR006061; SBP\_dom1.  
DR PROSITE; PS01037; SBP\_BACTERIAL\_1; PARTIAL.  
KW Transport; Sugar transport; Periplasmic.  
FT NON\_TER 1 1  
SQ SEQUENCE 10 AA; 1159 MW; 8FD8DC4415A6DDDA CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SR 3  
||  
Db 6 SR 7

RESULT 23

RT02\_BOVIN

ID RT02\_BOVIN STANDARD; PRT; 10 AA.  
AC P82923;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Mitochondrial 28S ribosomal protein S2 (MRP-S2) (Fragment).  
GN MRPS2.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=21276436; PubMed=11279123;  
RA Koc E.C., Burkhart W., Blackburn K., Moseley A., Sprenulli L.L.;  
RT "The small subunit of the mammalian mitochondrial ribosome:  
RT identification of the full complement of ribosomal proteins present.";  
RL J. Biol. Chem. 276:19363-19374(2001).  
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit  
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial.  
CC -!- SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.  
DR InterPro; IPR001865; Ribosomal\_S2.  
DR Pfam; PF00318; Ribosomal\_S2; PARTIAL.  
DR PROSITE; PS00962; RIBOSOMAL\_S2\_1; PARTIAL.  
KW Ribosomal protein; Mitochondrion.  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1246 MW; 6A7A6679C04B476B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 9 SR 10

RESULT 24

TKU1\_UREUN

ID TKU1\_UREUN STANDARD; PRT; 10 AA.  
AC P40751;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Urechistachykinin I.  
OS Urechis unicinctus.

OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.  
 OX NCBI\_TaxID=6432;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Ventral nerve cord;  
 RX MEDLINE=93236558; PubMed=8476410;  
 RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;  
 RT "Two novel tachykinin-related neuropeptides in the echiuroid worm,  
 RT Urechis unicinctus.";  
 RL Biochem. Biophys. Res. Commun. 192:1-6(1993).  
 CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL  
 CC MUSCLE OF THE ANIMAL.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1177 MW; C6D1C462C9D6C5A6 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 9 SR 10

#### RESULT 25

##### CORZ\_PERAM

ID CORZ\_PERAM STANDARD; PRT; 11 AA.  
 AC P11496;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Corazonin.  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=89325572; PubMed=2753132;  
 RA Veenstra J.A.;  
 RT "Isolation and structure of corazonin, a cardioactive peptide from  
 RT the American cockroach.";  
 RL FEBS Lett. 250:231-234(1989).  
 CC -!- FUNCTION: CARDIOACTIVE PEPTIDE. CORAZONIN IS PROBABLY INVOLVED  
 CC IN THE PHYSIOLOGICAL REGULATION OF THE HEART BEAT.  
 DR PIR; S05002; S05002.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;



Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 6 SR 7

RESULT 26

FAR6\_PENMO

ID FAR6\_PENMO STANDARD; PRT; 11 AA.  
AC P83321;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).  
OS Penaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
RT of the giant tiger prawn Penaeus monodon."  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 11 11 AMIDATION.  
SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 8 RL 9

RESULT 27

PKC1\_CARMO

ID PKC1\_CARMO STANDARD; PRT; 11 AA.  
AC P82684;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).  
OS Carausius morosus (Indian stick insect).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;  
 OC Heteronemiidae; Carausius.  
 OX NCBI\_TaxID=7022;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Corpora cardiaca;  
 RA Predel R., Kellner R., Gaede G.;  
 RT "Myotropic neuropeptides from the retrocerebral complex of the stick  
 RT insect, Carausius morosus (Phasmatodea: Lonchodidae).";  
 RL Eur. J. Entomol. 96:275-278(1999).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
 ||  
 Db 10 RL 11

# RESULT 28

## LMT1\_LOCM1

ID LMT1\_LOCM1 STANDARD; PRT; 12 AA.  
 AC P22395;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 01-AUG-1991 (Rel. 19, Last annotation update)  
 DE Locustamyotropin 1 (LOM-MT-1).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=90341077; PubMed=1974346;  
 RA Schoofs L., Holman G.M., Hayes T.K., Tips A., Nachman R.J.,  
 RA Vandesande F., de Loof A.;  
 RT "Isolation, identification and synthesis of locustamyotropin  
 RT (Lom-MT), a novel biologically active insect peptide.";  
 RL Peptides 11:427-433(1990).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR PIR; A43975; A43975.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.

KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 12 12 AMIDATION.  
SQ SEQUENCE 12 AA; 1213 MW; D766C92722D6DDDD CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 11 RL 12

# RESULT 29

## PPK4\_PERAM

ID PPK4\_PERAM STANDARD; PRT; 12 AA.  
AC P82619;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-4 (Pea-PK-4) (YXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=Retrocerebral complex;  
RX MEDLINE=99212469; PubMed=10196736;  
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
RT "Differential distribution of pyrokinin-isoforms in cerebral and  
RT abdominal neurohemal organs of the American cockroach."  
RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
RN [2]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
RT the American cockroach."  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.  
CC -!- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 12 12 AMIDATION.  
SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FF42CAA1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 11 RL 12

# RESULT 30

PPK4\_PERFU

ID PPK4\_PERFU STANDARD; PRT; 12 AA.  
 AC P82690;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-4 (PEF-PK-4) (YXPRL-amide).  
 OS Periplaneta fuliginosa (Smokybrown cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=36977;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
 RT the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- MASS SPECTROMETRY: MW=1437.9; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; FALSE\_NEG.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 12 12 AMIDATION.  
 SQ SEQUENCE 12 AA; 1439 MW; F9B53049FF42CAA1 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
 ||  
 Db 11 RL 12

# RESULT 31

RR16\_GINBI

ID RR16\_GINBI STANDARD; PRT; 12 AA.  
 AC P36207;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Chloroplast 30S ribosomal protein S16 (Fragment).  
 GN RPS16.  
 OS Ginkgo biloba (Ginkgo).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.  
 OX NCBI\_TaxID=3311;  
 RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=95094313; PubMed=8001171;  
RA Richard M., Tremblay C., Bellemare G.;  
RT "Chloroplastic genomes of Ginkgo biloba and Chlamydomonas moewusii  
RT contain a chlB gene encoding one subunit of a light-independent  
RT protochlorophyllide reductase.";  
RL Curr. Genet. 26:159-165(1994).  
CC -!- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.  
CC -----  
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CC -----  
DR EMBL; U01531; AAA66977.1; -.  
DR HAMAP; MF\_00385; -; 1.  
DR InterPro; IPR000307; Ribosomal\_S16.  
DR PROSITE; PS00732; RIBOSOMAL\_S16; 1.  
KW Ribosomal protein; Chloroplast.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1488 MW; 6700EDAF9D033734 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 5 RL 6

# RESULT 32

## LMT4\_LOCFMI

ID LMT4\_LOCFMI STANDARD; PRT; 13 AA.  
AC P41490;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Locustamyotropin 4 (LOM-MT-4).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,  
RA de Loof A.;  
RT "Isolation, identification and synthesis of locustamyotropin III and  
RT IV, two additional neuropeptides of Locusta migratoria: members of the  
RT locustamyotropin peptide family.";  
RL Insect Biochem. Mol. Biol. 22:447-452(1992).  
CC -!- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY

CC (MYOTROPIC ACTIVITY). LOM-MT IV SEEMS TO BE A MORE POTENT MUSCLE  
 CC STIMULATOR THAN LOM-MT I, II AND III.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR PIR; B61620; B61620.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 13 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1553 MW; 20861943824D6698 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 1 RL 2

### RESULT 33

#### NEUT\_CAVPO

ID NEUT\_CAVPO STANDARD; PRT; 13 AA.  
 AC P32560;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neurotensin (NT).  
 GN NTS.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Small intestine;  
 RX MEDLINE=86248085; PubMed=3087775;  
 RA Shaw C., Thim L., Conlon J.M.;  
 RT "[Ser7]neurotensin: isolation from guinea pig intestine."  
 RL FEBS Lett. 202:187-192(1986).  
 CC -!- FUNCTION: Smooth muscle-contracting peptide.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.  
 DR PIR; A53608; A53608.  
 KW Vasoactive; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 13 AA; 1680 MW; 4C8314644C4115B3 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 7 SR 8

### RESULT 34

## ALYT\_ALYOB

ID AYT\_ALYOB STANDARD; PRT; 14 AA.  
 AC P08944;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Alytesin.  
 OS Alytes obstetricans (Midwife toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Discoglossidae; Alytes.  
 OX NCBI\_TaxID=8443;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=84131098; PubMed=6141890;  
 RA Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;  
 RT "Active peptides in the skins of one hundred amphibian species from  
 RT Australia and Papua New Guinea."  
 RL Comp. Biochem. Physiol. 77C:99-108(1984).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR InterPro; IPR000874; Bombesin.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation;  
 KW Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 14 14 AMIDATION.  
 SQ SEQUENCE 14 AA; 1554 MW; D3C4E4D3AF129666 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 3 RL 4

## RESULT 35

## KLPS\_SCARA

ID KLPS\_SCARA STANDARD; PRT; 14 AA.  
 AC P58396;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Kinin-like peptide-S (Fragment).  
 OS Scaptocosa raptoria (Spider).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
 OC Araneomorphae; Entelegynae; Lycosoidea; Lycosidae; Scaptocosa.  
 OX NCBI\_TaxID=180440;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=98267639; PubMed=9604280;

RA Ferreira L.A.F., Lucas S.M., Alves E.W., Hermann V.V., Reichl A.P.,  
 RA Habermehl G., Zingali R.B.;  
 RT "Isolation, characterization and biological properties of two  
 RT kinin-like peptides (peptide-S and peptide-R) from *Scaptocosa*  
 RT *raptoria* venom.";  
 RL Toxicon 36:31-39(1998).  
 CC -!- FUNCTION: Has kinin-like biological properties. Causes contraction  
 CC on the of mammalian ileum; relaxes the duodenum and increases the  
 CC capillary permeability.  
 KW Vasodilator.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1510 MW; E811E2E5D2EE27CA CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 1 RL 2

#### RESULT 36

##### LPER\_BACLI

ID LPER\_BACLI STANDARD; PRT; 14 AA.  
 AC Q04303;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Erythromycin resistance leader peptide (23S rRNA methylase leader  
 DE peptide).  
 OS *Bacillus licheniformis*, and  
 OS *Bacillus anthracis*.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.  
 OX NCBI\_TaxID=1402, 1392;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*B.licheniformis*;  
 RX MEDLINE=84245158; PubMed=6429477;  
 RA Gryczan T., Israeli-Reches M., del Bue M., Dubnau D.;  
 RT "DNA sequence and regulation of *ermD*, a macrolide-lincosamide-  
 RT streptogramin B resistance element from *Bacillus licheniformis*."  
 RL Mol. Gen. Genet. 194:349-356(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*B.licheniformis*; STRAIN=EMR-1;  
 RX MEDLINE=91310580; PubMed=1713206;  
 RA Kwak J.-K., Choi E.-C., Weisblum B.;  
 RT "Transcriptional attenuation control of *ermK*, a  
 RT macrolide-lincosamide-streptogramin B resistance determinant from  
 RT *Bacillus licheniformis*."  
 RL J. Bacteriol. 173:4725-4735(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=*B.anthraxis*; STRAIN=590;  
 RX MEDLINE=93232776; PubMed=8473865;  
 RA Kim H.-S., Choi E.-C., Kim B.-K.;



RT "A macrolide-lincosamide-streptogramin B resistance determinant from  
RT Bacillus anthracis 590: cloning and expression of ermJ.";  
RL J. Gen. Microbiol. 139:601-607(1993).  
CC -!- FUNCTION: THIS PEPTIDE IS INVOLVED IN THE CONTROL MECHANISM OF  
CC THE SYNTHESIS OF THE MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B  
CC RESISTANCE PROTEIN. IT ACTS AS A TRANSCRIPTIONAL ATTENUATOR.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; L08389; AAA22596.1; -.  
DR EMBL; M29832; AAA22598.1; -.  
DR PIR; A42473; A42473.  
KW Antibiotic resistance; Leader peptide.  
SQ SEQUENCE 14 AA; 1732 MW; 5D1138B59F32ED07 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

#### RESULT 37

##### PPK6\_PERAM

ID PPK6\_PERAM STANDARD; PRT; 14 AA.  
AC P82693;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Pyrokinin-6 (Pea-PK-6) (FXPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.  
RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Eckert M.;  
RT "Tagma-specific distribution of FXPRLamides in the nervous system of  
RT the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -!- FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.  
CC -!- TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN  
CC ABDOMINAL PERISYMPATHETIC ORGANS.  
CC -!- MASS SPECTROMETRY: MW=1590.8; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR InterPro; IPR001484; Pyrokinin.

DR PROSITE; PS00539; PYROKININ; 1.  
 KW Amidation; Pyrokinin.  
 FT MOD\_RES 14 14 AMIDATION.  
 SQ SEQUENCE 14 AA; 1592 MW; 3966CC3FF384A998 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 13 RL 14

# RESULT 38

## SAP2\_ARBPU

ID SAP2\_ARBPU STANDARD; PRT; 14 AA.  
 AC P11760;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE Resact (Sperm-activating peptide) (SAP-IIA).  
 OS Arbacia punctulata (Punctuate sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Arbacoida; Arbaciidae; Arbacia.  
 OX NCBI\_TaxID=7641;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Egg;  
 RX MEDLINE=85054981; PubMed=6150045;  
 RA Suzuki N., Shimomura H., Radany E.W., Ramarao C.S., Ward G.E.,  
 RA Bentley J.K., Garbers D.L.;  
 RT "A peptide associated with eggs causes a mobility shift in a major  
 RT plasma membrane protein of spermatozoa.";  
 RL J. Biol. Chem. 259:14874-14879(1984).  
 RN [2]  
 RP DISULFIDE BOND.  
 RX MEDLINE=92097763; PubMed=1756858;  
 RA Yoshimo K.-I., Takao T., Shimonishi Y., Suzuki N.;  
 RT "Determination of the amino acid sequence of an intramolecular  
 RT disulfide linkage-containing sperm-activating peptide by tandem mass  
 RT spectrometry.";  
 RL FEBS Lett. 294:179-182(1991).  
 CC -!- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY  
 CC THROUGH INTRACELLULAR ALKALINIZATION, TRANSIENT ELEVATIONS OF  
 CC CAMP, CGMP AND CLACIUM LEVELS IN SPERM CELLS, AND TRANSIENT  
 CC ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF  
 CC GUANYLATE CYCLASE.  
 CC -!- SIMILARITY: SMALL TO S.PURPURATUS SPERACT.  
 KW Amidation.  
 FT DISULFID 1 8  
 FT MOD\_RES 14 14 AMIDATION.  
 SQ SEQUENCE 14 AA; 1246 MW; 39745AA33EBE41B8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 13 RL 14

RESULT 39

CX3B\_CONQU

ID CX3B\_CONQU STANDARD; PRT; 15 AA.  
AC P58842;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Conotoxin QcIIIB.  
OS Conus quercinus (Oak cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=101313;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90327072; PubMed=2165278;  
RA Abogadie F.C., Ramilo C.A., Corpuz G.P., Cruz L.J.;  
RL Unpublished results, cited by:  
RL Olivera B.M., Rivier J.E., Clark C., Ramilo C.A., Corpuz G.P.,  
RL Abogadie F.C., Mena E.E., Woodward S.R., Hillyard D.R., Cruz L.J.;  
RL Science 249:257-263(1990).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.  
KW Toxin; Hydroxylation.  
FT DISULFID 1 9 PROBABLE.  
FT DISULFID 2 12 PROBABLE.  
FT DISULFID 6 13 PROBABLE.  
FT MOD\_RES 11 11 HYDROXYLATION.  
SQ SEQUENCE 15 AA; 1724 MW; C9CEBA917BED832D CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 3 SR 4

RESULT 40

RS10\_BACST

ID RS10\_BACST STANDARD; PRT; 15 AA.  
AC P59683;  
DT 15-SEP-2003 (Rel. 42, Created)  
DT 15-SEP-2003 (Rel. 42, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE 30S ribosomal protein S10 (BS13) (Fragment).  
GN RPSJ.  
OS Bacillus stearothermophilus.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.

OX NCBI\_TaxID=1422;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=10;  
 RX PubMed=4607606;  
 RA Yaguchi M., Matheson A.T., Visentin L.P.;  
 RT "Procaryotic ribosomal proteins: N-terminal sequence homologies and  
 RT structural correspondence of 30 S ribosomal proteins from Escherichia  
 RT coli and Bacillus stearothermophilus.";  
 RL FEBS Lett. 46:296-300(1974).  
 CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By  
 CC similarity).  
 CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.  
 DR HAMAP; MF\_00508; -; 1.  
 DR PROSITE; PS00361; RIBOSOMAL\_S10; PARTIAL.  
 KW Ribosomal protein.  
 FT INIT\_MET 0 0  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1897 MW; 746B2ACEAF9AC031 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 8 RL 9

#### RESULT 41

TAl\_TREBR  
 ID TAl\_TREBR STANDARD; PRT; 15 AA.  
 AC P34070;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Tremmerogen A-I.  
 OS Tremella brasiliensis (Jelly fungus).  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Tremella.  
 OX NCBI\_TaxID=29896;  
 RN [1]  
 RP SEQUENCE.  
 RA Ishibashi Y., Sakagami Y., Isogai A., Suzuki A.;  
 RT "Structures of Tremmerogens A-9291-I and A-9291-VIII: peptidyl sex  
 RT hormones of Tremella brasiliensis.";  
 RL Biochemistry 23:1399-1404(1984).  
 CC -!- FUNCTION: TREMEROGEN A-I IS PRODUCED BY THE A MATING-TYPE CELLS  
 CC AND INDUCES FORMATION OF CONJUGATION TUBES IN A MATING-TYPE CELLS.  
 KW Pheromone; Prenylation; Lipoprotein.  
 FT LIPID 15 15 FARNESYL.  
 SQ SEQUENCE 15 AA; 1339 MW; 3AABA4FC2D605333 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            2 SR 3  
              ||  
Db            5 SR 6

RESULT 42

UC13\_MAIZE

ID UC13\_MAIZE        STANDARD;        PRT;    15 AA.  
AC P80619;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 243)  
DE (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
RT genome analysis program.";  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.8, ITS MW IS: 56.9 kDa.  
CC -!- SIMILARITY: TO GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASES.  
DR Maize-2DPAGE; P80619; COLEOPTILE.  
DR MaizeDB; 123946; -.  
FT NON\_TER        1        1  
FT NON\_TER        15       15  
SQ SEQUENCE    15 AA;   1739 MW;   02038EE7471AE038 CRC64;

Query Match                    40.0%; Score 2; DB 1; Length 15;  
Best Local Similarity    100.0%; Pred. No. 3.7e+03;  
Matches        2; Conservative    0; Mismatches    0; Indels        0; Gaps        0;

Qy            3 RL 4  
              ||  
Db            9 RL 10

RESULT 43

UC25\_MAIZE

ID UC25\_MAIZE        STANDARD;        PRT;    15 AA.  
AC P80631;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 77)  
DE (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9, ITS MW IS: 31.6 kDa.  
 DR Maize-2DPAGE; P80631; COLEOPTILE.  
 DR MaizeDB; 123957; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1580 MW; 83C54CF0CE1614D0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 6 SR 7

#### RESULT 44

URE1\_MORMO  
 ID URE1\_MORMO STANDARD; PRT; 15 AA.  
 AC P17337;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase) (Urease 63 kDa  
 DE subunit) (Fragment).  
 GN UREC.  
 OS Morganella morganii (Proteus morganii).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Morganella.  
 OX NCBI\_TaxID=582;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90264298; PubMed=2345135;  
 RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;  
 RT "Morganella morganii urease: purification, characterization, and  
 RT isolation of gene sequences.";  
 RL J. Bacteriol. 172:3073-3080(1990).  
 CC -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).  
 CC -!- COFACTOR: Binds 2 nickel ions per subunit (Potential).  
 CC -!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE UREASE FAMILY.  
 DR PIR; A35389; A35389.  
 DR InterPro; IPR005848; UreaseA.  
 DR PROSITE; PS00145; UREASE\_2; PARTIAL.  
 DR PROSITE; PS01120; UREASE\_1; PARTIAL.  
 KW Hydrolase; Metal-binding; Nickel.

FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1650 MW; 09E27AA54241687B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 4 SR 5

#### RESULT 45

##### AF2S\_MALPA

ID AF2S\_MALPA STANDARD; PRT; 16 AA.  
AC P83142;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Antifungal protein 2 small subunit (CW-2) (Fragment).  
OS Malva parviflora (Little mallow) (Cheeseweed).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.  
OX NCBI\_TaxID=145753;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Seed;  
RX MEDLINE=20568734; PubMed=11118343;  
RA Wang X., Bunkers G.J.;  
RT "Potent heterologous antifungal proteins from cheeseweed (Malva  
parviflora).";  
RL Biochem. Biophys. Res. Commun. 279:669-673(2000).  
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but  
CC not F.graminearum.  
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.  
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
CC concentration.  
DR GO; GO:0003799; F:antifungal peptide activity; IDA.  
KW Fungicide; Antibiotic.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 2027 MW; 9998D9EB8FB7EE65 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
||  
Db 4 SR 5

#### RESULT 46

##### FOR1\_MYRGU

ID FOR1\_MYRGU STANDARD; PRT; 16 AA.  
AC P81438;  
DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Formaecin 1.  
 OS *Myrmecia gulosa* (Red bulldog ant).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;  
 OC Myrmeciinae; Myrmecia.  
 OX NCBI\_TaxID=36170;  
 RN [1]  
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=98165787; PubMed=9497332;  
 RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;  
 RT "Isolation from an ant *Myrmecia gulosa* of two inducible  
 RT O-glycosylated proline-rich antibacterial peptides."  
 RL J. Biol. Chem. 273:6139-6143(1998).  
 CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI  
 CC BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE  
 CC BACTERIA.  
 CC -!- INDUCTION: By bacterial infection.  
 CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-  
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.  
 CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.  
 KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.  
 FT CARBOHYD 11 11 O-LINKED (GALNAC. . .).  
 SQ SEQUENCE 16 AA; 1794 MW; 80CEA3AABBC2E0AE CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 15 RL 16

#### RESULT 47

##### FOR2\_MYRGU

ID FOR2\_MYRGU STANDARD; PRT; 16 AA.  
 AC P81437;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Formaecin 2.  
 OS *Myrmecia gulosa* (Red bulldog ant).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;  
 OC Myrmeciinae; Myrmecia.  
 OX NCBI\_TaxID=36170;  
 RN [1]  
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE THR-11.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=98165787; PubMed=9497332;  
 RA Mackintosh J.A., Veal D.A., Beattie A.J., Gooley A.A.;  
 RT "Isolation from an ant *Myrmecia gulosa* of two inducible  
 RT O-glycosylated proline-rich antibacterial peptides."  
 RL J. Biol. Chem. 273:6139-6143(1998).



CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE. HAS ACTIVITY AGAINST E.COLI  
 CC BUT NONE AGAINST OTHER GRAM-NEGATIVE BACTERIA AND GRAM-POSITIVE  
 CC BACTERIA.  
 CC -!- INDUCTION: By bacterial infection.  
 CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-  
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.  
 CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.  
 KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.  
 FT CARBOHYD 11 11 O-LINKED (GALNAC. . .).  
 SQ SEQUENCE 16 AA; 1807 MW; 9C3CA3B00BC2E0AE CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 15 RL 16

#### RESULT 48

##### LPK1\_LOCF1

ID LPK1\_LOCF1 STANDARD; PRT; 16 AA.  
 AC P20404;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Locustapyrokinin 1 (LOM-PK-1).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=91224474; PubMed=2026322;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
 RT "Isolation, primary structure, and synthesis of locustapyrokinin: a  
 RT myotropic peptide of Locusta migratoria."  
 RL Gen. Comp. Endocrinol. 81:97-104(1991).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR PIR; A49761; A49761.  
 DR InterPro; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; 1.  
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 16 16 AMIDATION.  
 SQ SEQUENCE 16 AA; 1827 MW; A7178BBDCA0AFDD6 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4

Db                   ||  
15 RL 16

RESULT 49

PGTL\_PELAC

ID PGTL\_PELAC           STANDARD;           PRT;     16 AA.  
AC P80563;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Pyrogallol hydroxyltransferase large subunit (EC 1.97.1.2)  
DE (Transhydroxylase) (Fragment).  
OS Pelobacter acidigallici.  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;  
OC Pelobacteraceae; Pelobacter.  
OX NCBI\_TaxID=35816;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=DSM 2377 / Braunschweig;  
RX MEDLINE=96215436; PubMed=8647079;  
RA Reichenbecher W., Ruediger A., Kroneck P.M.H., Schink B.;  
RT "One molecule of molybdopterin guanine dinucleotide is associated  
RT with each subunit of the heterodimeric Mo-Fe-S protein  
RT transhydroxylase of Pelobacter acidigallici as determined by SDS/PAGE  
RT and mass spectrometry.";  
RL Eur. J. Biochem. 237:406-413(1996).  
CC -!- CATALYTIC ACTIVITY: 1,2,3,5-tetrahydroxybenzene + 1,2,3-  
CC trihydroxybenzene = 1,3,5-trihydroxybenzene + 1,2,3,5-  
CC tetrahydroxybenzene.  
CC -!- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).  
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.  
DR PIR; S65430; S65430.  
KW Oxidoreductase; Molybdenum; Iron-sulfur.  
FT NON\_TER           16       16  
SQ SEQUENCE    16 AA;   1620 MW;   56348D53A0AD6EE3 CRC64;

Query Match                   40.0%;   Score 2;   DB 1;   Length 16;  
Best Local Similarity   100.0%;   Pred. No. 3.9e+03;  
Matches       2;   Conservative       0;   Mismatches       0;   Indels       0;   Gaps       0;

Qy                   3 RL 4  
                      ||  
Db                   5 RL 6

RESULT 50

YMOR\_PSEPU

ID YMOR\_PSEPU           STANDARD;           PRT;     16 AA.  
AC Q02210;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein in morA 3'region (Fragment).  
OS Pseudomonas putida.  
OG Plasmid pMDH7.2.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=M10;  
 RX MEDLINE=93199531; PubMed=8452544;  
 RA Willey D.L., Caswell D.A., Lowe C.R., Bruce N.C.;  
 RT "Nucleotide sequence and over-expression of morphine dehydrogenase, a  
 RT plasmid-encoded gene from Pseudomonas putida M10.";  
 RL Biochem. J. 290:539-544(1993).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; M94775; AAB17357.1; -.  
 DR PIR; S30384; S30384.  
 KW Hypothetical protein; Plasmid.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1962 MW; A2F1EB8C172766ED CRC64;

Query Match 40.0%; Score 2; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 9 SR 10

Search completed: November 28, 2003, 14:31:18  
 Job time : 13 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:27:18 ; Search time 33 Seconds  
 (without alignments)  
 39.099 Million cell updates/sec

Title: US-09-228-866-45  
 Perfect score: 5  
 Sequence: 1 XSRLX 5

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8701

Minimum DB seq length: 5

Maximum DB seq length: 23

Post-processing: Listing first 100 summaries

Database : SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertibrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
1	3	60.0	9	4	Q9UC36	Q9uc36 homo sapien	
2	3	60.0	10	15	Q8UT83	Q8ut83 human immun	
3	3	60.0	11	2	P77404	P77404 escherichia	
4	3	60.0	13	6	Q9TRW6	Q9trw6 bos taurus	
5	3	60.0	14	2	P83159	P83159 anabaena sp	
6	3	60.0	15	4	P78533	P78533 homo sapien	
7	3	60.0	16	4	Q9UP51	Q9up51 homo sapien	
8	3	60.0	16	4	Q96RT5	Q96rt5 homo sapien	
9	3	60.0	18	6	O46592	O46592 capra hircu	
10	3	60.0	19	4	Q96ER8	Q96er8 homo sapien	
11	3	60.0	19	5	Q8T8B6	Q8t8b6 ciona intes	
12	3	60.0	19	6	Q95J98	Q95j98 sus scrofa	
13	3	60.0	19	10	Q8GS32	Q8gs32 hordeum vul	
14	3	60.0	20	13	Q9PRV5	Q9prv5 xenopus lae	
15	3	60.0	21	2	Q9R4R7	Q9r4r7 streptomyce	
16	3	60.0	21	2	Q9R890	Q9r890 chlamydia t	
17	3	60.0	21	2	Q53014	Q53014 rhizobium e	
18	3	60.0	21	4	Q96D65	Q96d65 homo sapien	
19	3	60.0	21	11	Q9ESX0	Q9esx0 mus musculu	
20	3	60.0	22	4	O15289	O15289 homo sapien	
21	3	60.0	22	4	Q96Q47	Q96q47 homo sapien	

22	3	60.0	22	11	Q9JLD6	Q9jld6 mesocricetu
23	3	60.0	22	12	Q84172	Q84172 orf virus.
24	3	60.0	23	2	Q9ZG66	Q9zg66 chlamydia t
25	3	60.0	23	2	O86987	O86987 proteus mir
26	3	60.0	23	4	Q9UC00	Q9uc00 homo sapien
27	2	40.0	6	10	P82181	P82181 spinacia ol
28	2	40.0	6	10	P82182	P82182 spinacia ol
29	2	40.0	7	2	O50556	O50556 actinobacil
30	2	40.0	7	8	P92214	P92214 amblyopyrum
31	2	40.0	7	8	P92393	P92393 hordeum vul
32	2	40.0	7	8	P92403	P92403 lophopyrum
33	2	40.0	7	8	P92427	P92427 peridictyon
34	2	40.0	7	8	P92430	P92430 aegilops ta
35	2	40.0	7	8	P92221	P92221 bromus iner
36	2	40.0	7	8	P92425	P92425 pseudoroegn
37	2	40.0	7	8	P92381	P92381 hordeum bra
38	2	40.0	7	8	P92387	P92387 henrardia p
39	2	40.0	7	8	P92210	P92210 agropyron c
40	2	40.0	7	8	P92440	P92440 thinopyrum
41	2	40.0	7	8	P92218	P92218 australopyr
42	2	40.0	7	8	P92390	P92390 heteranthel
43	2	40.0	7	8	P92372	P92372 haynaldia v
44	2	40.0	7	8	P92442	P92442 taeniatheru
45	2	40.0	7	8	P92226	P92226 crithopsis
46	2	40.0	7	8	P92385	P92385 hordeum mar
47	2	40.0	7	8	P92421	P92421 psathyrosta
48	2	40.0	7	10	P93233	P93233 lycopersico
49	2	40.0	8	2	P72279	P72279 rhodococcus
50	2	40.0	8	2	Q934S4	Q934s4 thiobacillu
51	2	40.0	8	2	Q51594	Q51594 escherichia
52	2	40.0	8	4	Q15898	Q15898 homo sapien
53	2	40.0	8	4	Q15888	Q15888 homo sapien
54	2	40.0	8	4	Q8TF70	Q8tf70 homo sapien
55	2	40.0	8	5	O15899	O15899 babesia ovi
56	2	40.0	8	5	Q94623	Q94623 manduca sex
57	2	40.0	8	8	O19957	O19957 gossypium h
58	2	40.0	8	8	O19961	O19961 gossypium d
59	2	40.0	8	8	O19958	O19958 gossypium b
60	2	40.0	8	8	Q9T4Y2	Q9t4y2 asterina pe
61	2	40.0	8	8	O19960	O19960 gossypium m
62	2	40.0	8	8	O19959	O19959 gossypium t
63	2	40.0	8	8	O19956	O19956 gossypium a
64	2	40.0	8	11	Q9ET18	Q9et18 mus spretus
65	2	40.0	8	11	Q8R5M9	Q8r5m9 mus musculu
66	2	40.0	8	11	Q99P40	Q99p40 mus musculu
67	2	40.0	8	11	Q9ET17	Q9et17 mus caroli
68	2	40.0	8	11	Q9ET16	Q9et16 mesocricetu
69	2	40.0	8	12	O89965	O89965 polyomaviru
70	2	40.0	9	2	Q45852	Q45852 clostridium
71	2	40.0	9	2	Q51765	Q51765 pseudomonas
72	2	40.0	9	4	Q9UKJ6	Q9ukj6 homo sapien
73	2	40.0	9	4	Q14715	Q14715 homo sapien
74	2	40.0	9	4	Q9UE26	Q9ue26 homo sapien
75	2	40.0	9	5	Q9TWD6	Q9twd6 leptinotars
76	2	40.0	9	8	Q9TKF2	Q9tkf2 asteromyrtu
77	2	40.0	9	8	Q9TLM7	Q9tlm7 laurencia v
78	2	40.0	9	8	Q9TKG1	Q9tkg1 calothamnus

79	2	40.0	9	11	O88889	O88889 mus musculu
80	2	40.0	9	12	P90359	P90359 barley mild
81	2	40.0	9	12	Q8QVD3	Q8qvd3 ovine respi
82	2	40.0	9	12	Q69349	Q69349 herpes simp
83	2	40.0	9	12	Q9IBM8	Q9ibm8 simian viru
84	2	40.0	9	12	Q9PYK1	Q9pyk1 simian viru
85	2	40.0	9	15	O12096	O12096 caprine art
86	2	40.0	9	15	O12100	O12100 caprine art
87	2	40.0	9	15	O12102	O12102 caprine art
88	2	40.0	9	15	O12098	O12098 caprine art
89	2	40.0	9	15	O12104	O12104 caprine art
90	2	40.0	9	15	Q64972	Q64972 avian rous-
91	2	40.0	10	2	Q50032	Q50032 mycobacteri
92	2	40.0	10	4	Q9UCU6	Q9ucu6 homo sapien
93	2	40.0	10	5	Q8WPE7	Q8wpe7 skogsbergia
94	2	40.0	10	6	Q8SPN8	Q8spn8 macaca mula
95	2	40.0	10	8	Q9TKF7	Q9tkf7 agonis gran
96	2	40.0	10	8	Q9TKF9	Q9tkf9 melaleuca v
97	2	40.0	10	8	Q9TKG2	Q9tkg2 callistemon
98	2	40.0	10	8	Q9TKF5	Q9tkf5 agonis spat
99	2	40.0	10	8	Q9TKF1	Q9tkf1 homalosperm
100	2	40.0	10	8	Q9TKF8	Q9tkf8 tristaniops

# ALIGNMENTS

## RESULT 1

Q9UC36

ID Q9UC36 PRELIMINARY; PRT; 9 AA.  
AC Q9UC36;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE 28 kDa heat shock protein homolog fragment 1 (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92218434; PubMed=1560006;  
RA Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;  
RT "Copurification of small heat shock protein with alpha B crystallin  
RT from human skeletal muscle.";  
RL J. Biol. Chem. 267:7718-7725(1992).  
FT NON\_TER 1 1  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F77B43 CRC64;

Query Match 60.0%; Score 3; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 6 SRL 8

# RESULT 2

Q8UT83

ID Q8UT83 PRELIMINARY; PRT; 10 AA.  
 AC Q8UT83;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Vpu protein.  
 GN VPU.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=00BW1795.6;  
 RA Novitsky V.A., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,  
 RA Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., Thior I.,  
 RA Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F.,  
 RA Marlink R., Lee T.-H., Essex M.;  
 RT "HIV-1 subtype C molecular phylogeny: consensus sequence for an AIDS  
 RT vaccine design."  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF443097; AAL34766.1; -.  
 SQ SEQUENCE 10 AA; 1264 MW; 91E52CB33321B37A CRC64;

Query Match 60.0%; Score 3; DB 15; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 8 SRL 10

# RESULT 3

P77404

ID P77404 PRELIMINARY; PRT; 11 AA.  
 AC P77404;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE DNA sequence downstream of the ECOPRRI HSD locus (Fragment).  
 GN HSDR.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97206151; PubMed=9157244;  
 RA Tyndall C., Lehnherr H., Sandmeier U., Kulik E., Bickle T.A.;  
 RT "The type IC hsd loci of the enterobacteria are flanked by DNA with  
 RT high homology to the phage P1 genome: implications for the evolution  
 RT and spread of DNA restriction systems."  
 RL Mol. Microbiol. 23:729-736(1997).

DR EMBL; X98145; CAA66840.1; -.  
DR EMBL; X98144; CAA66839.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 11 AA; 1259 MW; 714AB092A4072734 CRC64;

Query Match 60.0%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 3 SRL 5

#### RESULT 4

Q9TRW6

ID Q9TRW6 PRELIMINARY; PRT; 13 AA.  
AC Q9TRW6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE 25 kDa protein P25, peptide F3 (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91372400; PubMed=1909972;  
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,  
RA Shiratsuchi A., Uchida T., Imahori K.;  
RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a  
RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";  
RL FEBS Lett. 289:37-43(1991).  
FT NON\_TER 1 1  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1375 MW; 2C2822494805D1B7 CRC64;

Query Match 60.0%; Score 3; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 9 SRL 11

#### RESULT 5

P83159

ID P83159 PRELIMINARY; PRT; 14 AA.  
AC P83159;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Phycobilisome 32.1 kDa linker polypeptide, phycocyanin-associated,  
DE rod (Fragment).



OS Anabaena sp. (strain L31).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
 OX NCBI\_TaxID=29412;  
 RN [1]  
 RP SEQUENCE.  
 RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;  
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: ROD LINKER PROTEIN, ASSOCIATED WITH PHYCOCYANIN. LINKER  
 CC POLYPEPTIDES DETERMINE THE STATE OF AGGREGATION AND THE LOCATION  
 CC OF THE DISC-SHAPED PHYCOBILIPROTEIN UNITS WITHIN THE PHYCOBILISOME  
 CC AND MODULATE THEIR SPECTROSCOPIC PROPERTIES IN ORDER TO MEDIATE A  
 CC DIRECTED AND OPTIMAL ENERGY TRANSFER.  
 CC -!- SUBCELLULAR LOCATION: THIS PROTEIN OCCURS IN THE ROD, IT IS  
 CC ASSOCIATED WITH PHYCOCYANIN (BY SIMILARITY).  
 CC -!- SIMILARITY: TO OTHER PHYCOBILISOME LINKER PROTEINS.  
 KW Phycobilisome; Photosynthesis.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1405 MW; 96823E44F60A3115 CRC64;

Query Match 60.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 7 SRL 9

# RESULT 6

P78533

ID P78533 PRELIMINARY; PRT; 15 AA.  
 AC P78533;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Deoxyguanosine kinase (EC 2.7.1.113) (Fragment).  
 GN DGK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Johansson M., Karlsson A.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; U62042; AAB48932.1; -.  
 KW Kinase; Transferase.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1706 MW; 53575609CC614F8E CRC64;

Query Match 60.0%; Score 3; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 9 SRL 11

# RESULT 7

Q9UP51

ID Q9UP51 PRELIMINARY; PRT; 16 AA.  
AC Q9UP51;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Prolactin (Fragment).  
GN PROLACTIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84264464; PubMed=6146607;  
RA Takahashi H., Nabeshima Y., Nabeshima Y., Ogata K., Takeuchi S.;  
RT "Molecular cloning and nucleotide sequence of DNA complementary to  
RT human decidua prolactin mRNA.";  
RL J. Biochem. 95:1491-1499(1984).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Stevens F.R.A., Hajeer A., John S., Thomson W., Worthington J.,  
RA Davis J.R.E., Ollier W.E.R.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF068859; AAD12943.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1877 MW; 388F0E599FCA3F2F CRC64;

Query Match 60.0%; Score 3; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 9 SRL 11

# RESULT 8

Q96RT5

ID Q96RT5 PRELIMINARY; PRT; 16 AA.  
AC Q96RT5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Tuberous sclerosis 1 (Fragment).  
GN TSC1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fang L., Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Chao D.R.,

RA Fang Z.M.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF274227; AAK60414.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1826 MW; 895C250451E3BBEE CRC64;

Query Match 60.0%; Score 3; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 2 SRL 4

RESULT 9

O46592

ID O46592 PRELIMINARY; PRT; 18 AA.  
AC O46592;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Prolactin receptor short form (Fragment).  
OS Capra hircus (Goat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Caprinae; Capra.  
OX NCBI\_TaxID=9925;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98001468; PubMed=9343303;  
RA Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;  
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning  
RT and genomic analysis reveal that the two forms arise by different  
RT alternative splicing mechanisms in ruminants and in rodents.";  
RL J. Mol. Endocrinol. 19:109-120(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Bignon C.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF042781; AAB97749.1; -.  
KW Receptor.  
FT NON\_TER 1 1  
SQ SEQUENCE 18 AA; 2086 MW; 8C2297FA8816328D CRC64;

Query Match 60.0%; Score 3; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRL 4  
|||  
Db 12 SRL 14

RESULT 10

Q96ER8

ID Q96ER8 PRELIMINARY; PRT; 19 AA.  
 AC Q96ER8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis, and Embryonic carcinoma;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; BC011998; AAH11998.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 19 AA; 2180 MW; 137DB66BEE0B9B59 CRC64;  
  
 Query Match 60.0%; Score 3; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 SRL 4  
 |||  
 Db 11 SRL 13

RESULT 11

Q8T8B6

ID Q8T8B6 PRELIMINARY; PRT; 19 AA.  
 AC Q8T8B6;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Choline acetyltransferase (Fragment).  
 GN CI-CHAT.  
 OS Ciona intestinalis.  
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 OC Phlebobranchia; Cionidae; Ciona.  
 OX NCBI\_TaxID=7719;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21863848; PubMed=11875658;  
 RA Takamura K., Egawa T., Ohnishi S., Okada T., Fukuoka T.;  
 RT "Developmental expression of ascidian neurotransmitter synthesis  
 RT genesI. Choline acetyltransferase and acetylcholine transporter  
 RT genes.";  
 RL Dev. Genes Evol. 212:50-53(2002).  
 DR EMBL; AB072000; BAB85861.1; -.  
 KW Transferase.  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2176 MW; 36DC3BCDC6AB922F CRC64;

Query Match 60.0%; Score 3; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 15 SRL 17

RESULT 12

Q95J98

ID Q95J98 PRELIMINARY; PRT; 19 AA.  
AC Q95J98;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Laminin gamma 1 chain (Fragment).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cardiovascular;  
RA Markmann A., Kresse H.;  
RT "Regulation of VSMC Differentiation.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF330204; AAL09470.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2214 MW; 8D3245EE2DD7EB6C CRC64;

Query Match 60.0%; Score 3; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 11 SRL 13

RESULT 13

Q8GS32

ID Q8GS32 PRELIMINARY; PRT; 19 AA.  
AC Q8GS32;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE MLA13uORF 1.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Halterman D.A., Wei F., Wise R.P.;  
RT "Powdery mildew-induced Mla mRNAs are alternatively spliced and  
RT contain multiple upstream open reading frames.";

RL Plant Physiol. 0:0-0(2003).  
DR EMBL; AF523679; AAO16002.1; -.  
DR EMBL; AF523680; AAO16006.1; -.  
DR EMBL; AF523681; AAO16009.1; -.  
DR EMBL; AF523682; AAO16012.1; -.  
DR EMBL; AF523683; AAO16015.1; -.  
SQ SEQUENCE 19 AA; 2289 MW; 872EAC1EB20D2EAF CRC64;

Query Match 60.0%; Score 3; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 6 SRL 8

#### RESULT 14

Q9PRV5

ID Q9PRV5 PRELIMINARY; PRT; 20 AA.  
AC Q9PRV5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE NI(2+)-binding protein, PNIXB (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95000642; PubMed=7917276;  
RA Grbac-Ivankovic S., Antonijczuk K., Varghese A.H., Plowman M.C.,  
RA Antonijczuk A., Korza G., Ozols J., Sunderman F.W.Jr.;  
RT "Lipovitellin 2 beta is the 31 kD Ni(2+)-binding protein (pNiXb) in  
RT Xenopus oocytes and embryos."  
RL Mol. Reprod. Dev. 38:256-263(1994).  
SQ SEQUENCE 20 AA; 2318 MW; 9681AB6C0E5BAE44 CRC64;

Query Match 60.0%; Score 3; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 16 SRL 18

#### RESULT 15

Q9R4R7

ID Q9R4R7 PRELIMINARY; PRT; 21 AA.  
AC Q9R4R7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE CLAVAMINATE synthase isozyme 3 (Fragment).

OS Streptomyces antibioticus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1890;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95197540; PubMed=7890654;  
 RA Janc J.W., Egan L.A., Townsend C.A.;  
 RT "Purification and characterization of clavamate synthase from  
 RT Streptomyces antibioticus. A multifunctional enzyme of clavam  
 RT biosynthesis.";  
 RL J. Biol. Chem. 270:5399-5404(1995).  
 SQ SEQUENCE 21 AA; 2222 MW; E5012FAA658F5A5A CRC64;

Query Match 60.0%; Score 3; DB 2; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 18 SRL 20

# RESULT 16

Q9R890

ID Q9R890 PRELIMINARY; PRT; 21 AA.  
 AC Q9R890;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Hypothetical 2.3 kDa protein (Fragment).  
 OS Chlamydia trachomatis.  
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
 OX NCBI\_TaxID=813;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=L2 434B;  
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;  
 RT "Gene identification of Chlamydia trachomatis by random DNA  
 RT sequencing.";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF087312; AAD04087.1; -.  
 KW Hypothetical protein.  
 FT NON\_TER 21 21  
 SQ SEQUENCE 21 AA; 2346 MW; 5A282DC334CEB5EF CRC64;

Query Match 60.0%; Score 3; DB 2; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 9 SRL 11

# RESULT 17

Q53014

ID Q53014 PRELIMINARY; PRT; 21 AA.  
AC Q53014;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Nitrogenase alpha subunit (NifD) truncated (Fragment).  
OS Rhizobium etli.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium.  
OX NCBI\_TaxID=29449;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CE-3;  
RX MEDLINE=96236026; PubMed=8655489;  
RA Valderrama B., Davalos A., Girard L., Morett E., Mora J.;  
RT "Regulatory proteins and cis-acting elements involved in the  
RT transcriptional control of Rhizobium etli reiterated nifH genes.";  
RL J. Bacteriol. 178:3119-3126(1996).  
DR EMBL; L13618; AAB07744.1; -.  
FT NON\_TER 21 21  
SQ SEQUENCE 21 AA; 2490 MW; 19282319A357D445 CRC64;

Query Match 60.0%; Score 3; DB 2; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 16 SRL 18

# RESULT 18

Q96D65

ID Q96D65 PRELIMINARY; PRT; 21 AA.  
AC Q96D65;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC012895; AAH12895.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 21 AA; 2355 MW; 3F3C4E923AAB9327 CRC64;

Query Match 60.0%; Score 3; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4



Db

|||  
19 SRL 21

RESULT 19

Q9ESX0

ID Q9ESX0 PRELIMINARY; PRT; 21 AA.  
AC Q9ESX0;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Gephyrin (Fragment).  
GN GPHN OR GEPHYRIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20420367; PubMed=10963686;  
RA Ramming M., Kins S., Werner N., Hermann A., Betz H., Kirsch J.;  
RT "Diversity and phylogeny of gephyrin: Tissue-specific splice variants,  
RT gene structure, and sequence similarities to molybdenum cofactor-  
RT synthesizing and cytoskeleton-associated proteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:10266-10271(2000).  
DR EMBL; AJ278768; CAC06105.1; -.  
DR MGD; MGI:109602; Gphn.  
FT NON\_TER 1 1  
FT NON\_TER 21 21  
SQ SEQUENCE 21 AA; 2627 MW; 0820F760BC776F9A CRC64;

Query Match 60.0%; Score 3; DB 11; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 3 SRL 5

RESULT 20

O15289

ID O15289 PRELIMINARY; PRT; 22 AA.  
AC O15289;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Aldose reductase (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95309538; PubMed=7789640;  
RA Ko B.C., Lam K.S., Wat N.M., Chung S.S.;  
RT "An (A-C)n dinucleotide repeat polymorphic marker at the 5' end of the

RT aldose reductase gene is associated with early-onset diabetic  
 RT retinopathy in NIDDM patients.";  
 RL Diabetes 44:727-732(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ko B.C., Chung S.S.;  
 RT "Identification and characterization of multiple osmotic respnse  
 RT sequences in the aldose reductase gene.";  
 RL J. Biol. Chem. 272:0-0(1997).  
 DR EMBL; U72619; AAB61992.1; -.  
 DR HSSP; P15121; 2ACQ.  
 DR InterPro; IPR001395; Aldo/ket\_red.  
 DR Pfam; PF00248; aldo\_ket\_red; 1.  
 FT NON\_TER 22 22  
 SQ SEQUENCE 22 AA; 2385 MW; 3E3942ABB4061CB8 CRC64;

Query Match 60.0%; Score 3; DB 4; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 3 SRL 5

# RESULT 21

Q96Q47

ID Q96Q47 PRELIMINARY; PRT; 22 AA.  
 AC Q96Q47;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Mitochondrial ribosomal protein S2 (Fragment).  
 GN MRPS2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21429115; PubMed=11543634;  
 RA Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,  
 RA Watanabe K., Tanaka T.;  
 RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes  
 RT to the chromosomes and implications for human disorders.";  
 RL Genomics 77:65-70(2001).  
 DR EMBL; AB051627; BAB54954.1; -.  
 KW Ribosomal protein.  
 FT NON\_TER 22 22  
 SQ SEQUENCE 22 AA; 2565 MW; B8FA567A3A38F718 CRC64;

Query Match 60.0%; Score 3; DB 4; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||

Db

8 SRL 10

RESULT 22

Q9JLD6

ID Q9JLD6 PRELIMINARY; PRT; 22 AA.  
AC Q9JLD6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE P53 tumor suppressor (Fragment).  
OS Mesocricetus auratus (Golden hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Mesocricetus.  
OX NCBI\_TaxID=10036;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=20150266; PubMed=10684946;  
RA Laverdiere M., Beaudoin J., Lavigueur A.;  
RT "Species-specific regulation of alternative splicing in the C-terminal  
RT region of the p53 tumor suppressor gene.";  
RL Nucleic Acids Res. 28:1489-1497(2000).  
DR EMBL; AF190271; AAF43280.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 22 22  
SQ SEQUENCE 22 AA; 2550 MW; F1C22CB33A0B27D1 CRC64;

Query Match 60.0%; Score 3; DB 11; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4

|||

Db 11 SRL 13

RESULT 23

Q84172

ID Q84172 PRELIMINARY; PRT; 22 AA.  
AC Q84172;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Vaccinia virus E10R homolog (Fragment).  
OS Orf virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Parapoxvirus.  
OX NCBI\_TaxID=10258;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N72;  
RX MEDLINE=96335692; PubMed=8758000;  
RA Mercer A.A., Green G., Sullivan J.T., Robinson A.J., Drillien R.;  
RT "Location, DNA sequence and transcriptional analysis of the DNA  
RT polymerase gene of orf virus.";

RL J. Gen. Virol. 77:1563-1568(1996).  
DR EMBL; U49979; AAB19091.1; -.  
FT NON\_TER 22 22  
SQ SEQUENCE 22 AA; 2811 MW; 7D23D05E7C4F83A4 CRC64;

Query Match 60.0%; Score 3; DB 12; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 11 SRL 13

#### RESULT 24

Q9ZG66

ID Q9ZG66 PRELIMINARY; PRT; 23 AA.  
AC Q9ZG66;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)  
DE Virulence protein PGP7-D (Fragment).  
OS Chlamydia trachomatis.  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=813;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=L2 434B;  
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;  
RT "Gene identification of Chlamydia trachomatis by random DNA  
sequencing."  
RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AF087290; AAD04067.1; -.  
FT NON\_TER 23 23  
SQ SEQUENCE 23 AA; 2596 MW; 95DA4A282DC334CE CRC64;

Query Match 60.0%; Score 3; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
|||  
Db 9 SRL 11

#### RESULT 25

O86987

ID O86987 PRELIMINARY; PRT; 23 AA.  
AC O86987;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Yrfe (Fragment).  
GN YRFE.  
OS Proteus mirabilis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Proteus.

OX NCBI\_TaxID=584;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=U6450;  
 RX MEDLINE=98389307; PubMed=9723914;  
 RA Dufour A., Furness R.B., Hughes C.;  
 RT "Novel genes that upregulate the *Proteus mirabilis* flhDC master operon  
 RT controlling flagellar biogenesis and swarming.";  
 RL Mol. Microbiol. 29:741-752(1998).  
 DR EMBL; U66822; AAC28925.1; -.  
 FT NON\_TER 23 23  
 SQ SEQUENCE 23 AA; 2755 MW; 15866BCC4FED26DD CRC64;

Query Match 60.0%; Score 3; DB 2; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 18 SRL 20

# RESULT 26

Q9UC00

ID Q9UC00 PRELIMINARY; PRT; 23 AA.  
 AC Q9UC00;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Enhancement of wound HEALING process.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95130623; PubMed=7829572;  
 RA Pierschbacher M.D., Polarek J.W., Craig W.S., Tschopp J.F.,  
 RA Sipes N.J., Harper J.R.;  
 RL J. Cell. Biochem. 56:150-154(1994).  
 SQ SEQUENCE 23 AA; 2268 MW; CE73999CB9903891 CRC64;

Query Match 60.0%; Score 3; DB 4; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRL 4  
 |||  
 Db 15 SRL 17

# RESULT 27

P82181

ID P82181 PRELIMINARY; PRT; 6 AA.  
 AC P82181;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. ALWARO; TISSUE=Leaf;  
 RX MEDLINE=20435798; PubMed=10874046;  
 RA Yamaguchi K., Subramanian A.R.;  
 RT "The plastid ribosomal proteins. Identification of all the proteins in  
 RT the 50 S subunit of an organelle ribosome (chloroplast).";  
 RL J. Biol. Chem. 275:28466-28482(2000).  
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.  
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro; IPR001790; Ribosomal\_L10.  
 DR InterPro; IPR002363; Ribosomal\_L10eub.  
 DR Pfam; PF00466; Ribosomal\_L10; PARTIAL.  
 DR PROSITE; PS01109; RIBOSOMAL\_L10; PARTIAL.  
 KW Ribosomal protein; Chloroplast; rRNA-binding.  
 FT NON\_TER 6 6  
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 40.0%; Score 2; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 3 SR 4

#### RESULT 28

P82182

ID P82182 PRELIMINARY; PRT; 6 AA.  
 AC P82182;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. ALWARO; TISSUE=Leaf;  
 RX MEDLINE=20435798; PubMed=10874046;  
 RA Yamaguchi K., Subramanian A.R.;  
 RT "The plastid ribosomal proteins. Identification of all the proteins in  
 RT the 50 S subunit of an organelle ribosome (chloroplast).";

RL J. Biol. Chem. 275:28466-28482(2000).  
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.  
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro; IPR001790; Ribosomal\_L10.  
 DR InterPro; IPR002363; Ribosomal\_L10eub.  
 DR Pfam; PF00466; Ribosomal\_L10; PARTIAL.  
 DR PROSITE; PS01109; RIBOSOMAL\_L10; PARTIAL.  
 KW Ribosomal protein; Chloroplast; rRNA-binding.  
 FT NON\_TER 6 6  
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 40.0%; Score 2; DB 10; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 3 SR 4

#### RESULT 29

O50556

ID O50556 PRELIMINARY; PRT; 7 AA.  
 AC O50556;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE GlyA (Fragment).  
 GN GLYA.  
 OS Actinobacillus actinomycetemcomitans (Haemophilus  
 OS actinomycetemcomitans).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Actinobacillus.  
 OX NCBI\_TaxID=714;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 33384;  
 RX MEDLINE=96355846; PubMed=8751884;  
 RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,  
 RA Kraig E.;  
 RT "cis Elements and trans factors are both important in strain-specific  
 RT regulation of the leukotoxin gene in Actinobacillus  
 RT actinomycetemcomitans.";  
 RL Infect. Immun. 64:3451-3460(1996).  
 DR EMBL; U51862; AAB88721.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||

Db

2 RL 3

RESULT 30

P92214

ID P92214 PRELIMINARY; PRT; 7 AA.  
AC P92214;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Amblyopyrum muticum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Amblyopyrum.  
OX NCBI\_TaxID=4595;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5572; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77756; CAB01346.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

RESULT 31

P92393

ID P92393 PRELIMINARY; PRT; 7 AA.  
AC P92393;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Hordeum vulgare (Barley).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.



RC STRAIN=H3139; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77764; CAB01370.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

# RESULT 32

P92403

ID P92403 PRELIMINARY; PRT; 7 AA.  
AC P92403;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Lophopyrum.  
OX NCBI\_TaxID=4588;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6692; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77743; CAB01307.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

RESULT 33

P92427

ID P92427 PRELIMINARY; PRT; 7 AA.  
 AC P92427;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein (Fragment).  
 GN RPS11.  
 OS Peridictyon sanctum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Peridictyon.  
 OX NCBI\_TaxID=37683;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5575; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77749; CAB01325.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 6 RL 7

RESULT 34

P92430

ID P92430 PRELIMINARY; PRT; 7 AA.  
 AC P92430;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Aegilops tauschii (Aegilops squarrosa).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Aegilops.  
 OX NCBI\_TaxID=37682;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6668; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77758; CAB01352.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

RESULT 35  
P92221

ID P92221 PRELIMINARY; PRT; 7 AA.  
AC P92221;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Bromus inermis (Smooth brome grass).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Bromeae; Bromus.  
OX NCBI\_TaxID=15371;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OSA414; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77759; CAB01355.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

RESULT 36  
P92425

ID P92425 PRELIMINARY; PRT; 7 AA.

AC P92425;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Pseudoroegneria.  
 OX NCBI\_TaxID=4604;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H9082; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77744; CAB01310.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 6 RL 7

#### RESULT 37

P92381

ID P92381 PRELIMINARY; PRT; 7 AA.  
 AC P92381;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Hordeum brachyantherum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=52712;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).

DR EMBL; Z77761; CAB01361.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

#### RESULT 38

P92387

ID P92387 PRELIMINARY; PRT; 7 AA.  
AC P92387;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Henrardia persica.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Henrardia.  
OX NCBI\_TaxID=37678;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5556; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77748; CAB01322.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

#### RESULT 39

P92210

ID P92210 PRELIMINARY; PRT; 7 AA.  
AC P92210;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Agropyron cristatum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Agropyron.  
 OX NCBI\_TaxID=4593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H4349; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77771; CAB01391.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 6 RL 7

RESULT 40  
 P92440

ID P92440 PRELIMINARY; PRT; 7 AA.  
 AC P92440;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Thinopyrum bessarabicum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Thinopyrum.  
 OX NCBI\_TaxID=4601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6725; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77769; CAB01385.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1

SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
||  
Db 6 RL 7

RESULT 41

P92218

ID P92218 PRELIMINARY; PRT; 7 AA.  
AC P92218;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Australopyrum retrofractum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Australopyrum.  
OX NCBI\_TaxID=4597;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6723; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77767; CAB01379.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RL 4  
||  
Db 6 RL 7

RESULT 42

P92390

ID P92390 PRELIMINARY; PRT; 7 AA.  
AC P92390;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.

OS Heteranthelium piliferum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Heteranthelium.  
 OX NCBI\_TaxID=37679;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5557; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77750; CAB01328.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 6 RL 7

#### RESULT 43

P92372

ID P92372 PRELIMINARY; PRT; 7 AA.  
 AC P92372;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Haynaldia villosa.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Haynaldia.  
 OX NCBI\_TaxID=40247;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5561; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77741; CAB01301.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;



Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

RESULT 44

P92442

ID P92442 PRELIMINARY; PRT; 7 AA.  
AC P92442;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Taeniatherum caput-medusae (Medusahead).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Taeniatherum.  
OX NCBI\_TaxID=37687;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H10254; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77760; CAB01358.1; -.  
KW Chloroplast.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
||  
Db 6 RL 7

RESULT 45

P92226

ID P92226 PRELIMINARY; PRT; 7 AA.  
AC P92226;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Crithopsis delileana.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Crithopsis.  
 OX NCBI\_TaxID=37674;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5558; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data.";   
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77751; CAB01331.1; -.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 6 RL 7

#### RESULT 46

P92385

ID P92385 PRELIMINARY; PRT; 7 AA.  
 AC P92385; P92383;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Hordeum marinum (Seaside barley).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H299, and H801; TISSUE=Leaf;  
 RA Petersen G., Seberg O.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; Z77763; CAB01367.1; -.  
 DR EMBL; Z77762; CAB01364.1; -.  
 KW Chloroplast; Ribosomal protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||

Db

6 RL 7

RESULT 47

P92421

ID P92421 PRELIMINARY; PRT; 7 AA.  
AC P92421; P92419;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Psathyrostachys fragilis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Psathyrostachys.  
OX NCBI\_TaxID=37729;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H4372, and H917; TISSUE=Leaf;  
RA Petersen G., Seberg O.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; Z77753; CAB01337.1; -.  
DR EMBL; Z77752; CAB01334.1; -.  
KW Chloroplast; Ribosomal protein.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 894 MW; 6734140333277700 CRC64;

Query Match 40.0%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4

||

Db 6 RL 7

RESULT 48

P93233

ID P93233 PRELIMINARY; PRT; 7 AA.  
AC P93233;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)  
DE (Fragment).  
GN LE-ACS1B.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97351561; PubMed=9207843;  
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;

RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate  
 RT synthase genes by elicitor in suspension cultures of tomato  
 RT (Lycopersicon esculentum).";  
 RL Plant Mol. Biol. 34:275-286(1997).  
 DR EMBL; U75692; AAC49682.1; -.  
 KW Lyase.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match 40.0%; Score 2; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 1 SR 2

#### RESULT 49

P72279

ID P72279 PRELIMINARY; PRT; 8 AA.  
 AC P72279;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Biphenyl dioxygenase (Fragment).  
 GN BPHB.  
 OS Rhodococcus globerulus.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Nocardiaceae; Rhodococcus.  
 OX NCBI\_TaxID=33008;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255652; PubMed=7737502;  
 RA Asturias J.A., Diaz E., Timmis K.N.;  
 RT "Evolutionary relationship of the biphenyl dioxygenase of the gram-  
 RT positive bacterium Rhodococcus globerulus P6 to multicomponent  
 RT dioxygenases of gram-negative bacteria.";  
 RL Gene 156:11-18(1995).  
 DR EMBL; X80041; CAA56350.1; -.  
 KW Dioxygenase.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 989 MW; EBD2CB1AB6D73406 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RL 4  
 ||  
 Db 2 RL 3

#### RESULT 50

Q934S4

ID Q934S4 PRELIMINARY; PRT; 8 AA.  
 AC Q934S4;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MerD protein (Fragment).  
 GN MERD.  
 OS Thiobacillus ferrooxidans.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillus.  
 OX NCBI\_TaxID=920;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=G66; TRANSPOSON=Tn5037;  
 RA Kalyaeva E.S., Kholodii G.Y., Bass I.A., Gorlenko A.M., Yurieva O.V.,  
 RA Nikiforov V.G.;  
 RT "Tn5037, a Tn21-like mercury resistance transposon from Thiobacillus  
 RT ferrooxidans.";  
 RL Russ. J. Genet. 37:972-975(2001).  
 DR EMBL; AJ251743; CAC69252.1; -.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 937 MW; ED15A2D77B5DD446 CRC64;

Query Match 40.0%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SR 3  
 ||  
 Db 7 SR 8

Search completed: November 28, 2003, 14:32:06  
 Job time : 37 secs

OM protein - protein search, using sw model

Run on: November 28, 2003, 15:39:24 ; Search time 41 Seconds  
(without alignments)  
19.357 Million cell updates/sec

Title: US-09-228-866-46  
Perfect score: 5  
Sequence: 1 XVLRX 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 468892

Minimum DB seq length: 5  
Maximum DB seq length: 33

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03:\*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\*
- 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*
- 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\*
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- 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*
- 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:\*
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- 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*
- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3	60.0	5	8	AAP71643		Diuretic peptide d
2	3	60.0	5	16	AAR67200		Bovine glial cell
3	3	60.0	5	17	AAW09683		Cyclic pentapeptid
4	3	60.0	5	17	AAR86664		GGF II tryptic pep
5	3	60.0	5	18	AAW13413		Brain homing pepti
6	3	60.0	5	19	AAW51298		Human B-type natri
7	3	60.0	5	20	AAW97427		Shigella-like toxi
8	3	60.0	5	21	AAW80232		B-type natriuretic
9	3	60.0	5	21	AAW68290		Peptide SEQ ID NO:
10	3	60.0	5	21	AAW52944		MHC domain DR pept
11	3	60.0	5	22	AAU03880		G protein-coupled
12	3	60.0	5	22	AAU03881		G protein-coupled
13	3	60.0	5	22	AAB58705		Altered MHC determ
14	3	60.0	5	24	AAO19570		M sterilia protein
15	3	60.0	6	19	AAW51290		Human B-type natri
16	3	60.0	6	19	AAW56842		Enzyme inhibitor p
17	3	60.0	6	20	AAW55285		ATCC HB 11885 mono
18	3	60.0	6	21	AAW80220		Human B-type natri
19	3	60.0	6	21	AAW87031		Human haematopoiet
20	3	60.0	6	22	ABM00062		Savinas antibody b
21	3	60.0	6	22	ABM00074		Savinas antibody b
22	3	60.0	6	22	AAU03882		G protein-coupled
23	3	60.0	6	22	AAU03890		G protein-coupled
24	3	60.0	6	22	AAU03891		G protein-coupled
25	3	60.0	6	23	AAU97098		Abscisic acid (ABA
26	3	60.0	6	23	AAM47693		Human HARE peptide
27	3	60.0	7	19	AAW51299		Human B-type natri
28	3	60.0	7	20	AAW41942		Rheumatoid arthrit
29	3	60.0	7	20	AAW14768		P450 enzyme conser
30	3	60.0	7	20	AAW16932		Heat shock protein
31	3	60.0	7	20	AAW16976		Heat shock protein
32	3	60.0	7	21	AAW80233		B-type natriuretic
33	3	60.0	7	22	AAU72074		Melanoma antigen,
34	3	60.0	7	22	AAU72118		Melanoma antigen,
35	3	60.0	7	22	AAU03883		G protein-coupled
36	3	60.0	7	22	AAU03884		G protein-coupled
37	3	60.0	7	22	AAU03888		G protein-coupled
38	3	60.0	7	22	AAU03889		G protein-coupled
39	3	60.0	7	22	AAB98053		Rat endoproteinase
40	3	60.0	7	22	AAB88610		Human interleukin-
41	3	60.0	7	22	AAB88800		Human interleukin-
42	3	60.0	7	22	AAB49848		Human endostatin p
43	3	60.0	7	23	ABG77658		Targetting peptide
44	3	60.0	7	23	ABG77669		Targetting peptide
45	3	60.0	7	23	ABG77670		Targetting peptide
46	3	60.0	7	23	ABG77675		Targetting peptide
47	3	60.0	7	23	AAO17318		A thaliana recepto
48	3	60.0	7	23	AAU79912		Cassette mutagenes
49	3	60.0	7	23	AAU80624		Javelin peptide #5
50	3	60.0	7	23	AAU80668		Javelin peptide #9

51	3	60.0	8	16	AAR71108	Partial peptide of
52	3	60.0	8	18	AAW13414	Brain homing pepti
53	3	60.0	8	20	AAV40757	S5 derivative #10,
54	3	60.0	8	20	AAV16805	Heat shock protein
55	3	60.0	8	21	AAB30096	Scaffold protein S
56	3	60.0	8	21	AAB07390	Brain homing pepti
57	3	60.0	8	21	AAV69087	Subsequence which
58	3	60.0	8	22	AAE11796	Phage peptide #4 t
59	3	60.0	8	22	AAU03245	Fruit fly G protei
60	3	60.0	8	22	AAU03300	Fruit fly G protei
61	3	60.0	8	22	AAU03303	Fruit fly G protei
62	3	60.0	8	22	AAU03305	Fruit fly G protei
63	3	60.0	8	22	AAU03314	Fruit fly G protei
64	3	60.0	8	22	AAU03321	Fruit fly G protei
65	3	60.0	8	22	AAU03826	G protein-coupled
66	3	60.0	8	22	AAU03827	G protein-coupled
67	3	60.0	8	22	AAU03834	G protein-coupled
68	3	60.0	8	22	AAU03847	G protein-coupled
69	3	60.0	8	22	AAU03861	G protein-coupled
70	3	60.0	8	22	AAU03886	G protein-coupled
71	3	60.0	8	22	AAU03887	G protein-coupled
72	3	60.0	8	22	AAB88799	Human interleukin-
73	3	60.0	8	23	ABJ04395	HUVEC cell targeti
74	3	60.0	8	23	ABB76371	Haemophilus influe
75	3	60.0	8	23	AAE22082	Gasterosteus acule
76	3	60.0	8	23	AAU76990	Luteinizing hormon
77	3	60.0	8	23	AAU10707	Brain homing pepti
78	3	60.0	8	24	ABP74487	Human PRAME epitop
79	3	60.0	8	24	ABP75102	Proteome analysis
80	3	60.0	8	24	ABP75153	Proteome analysis
81	3	60.0	9	12	AAR14600	CMV gB epitope 559
82	3	60.0	9	15	AAV37966	Human cERB2 oncoge
83	3	60.0	9	18	AAW39634	Human p53 peptide
84	3	60.0	9	18	AAW39635	Human p53 peptide
85	3	60.0	9	18	AAW45677	c-ERB2 754 peptide
86	3	60.0	9	18	AAW32987	HIV nef protein ep
87	3	60.0	9	18	AAW13435	Brain homing pepti
88	3	60.0	9	18	AAW09897	Prostate specific
89	3	60.0	9	20	AAV45536	Immunogenic peptid
90	3	60.0	9	20	AAV46145	Immunogenic peptid
91	3	60.0	9	20	AAV46146	Immunogenic peptid
92	3	60.0	9	20	AAV46147	Immunogenic peptid
93	3	60.0	9	20	AAV46767	Immunogenic peptid
94	3	60.0	9	20	AAV46772	Immunogenic peptid
95	3	60.0	9	20	AAV47765	Immunogenic peptid
96	3	60.0	9	20	AAW97374	HA-1 R-allele sequ
97	3	60.0	9	20	AAW99197	Minor histocompati
98	3	60.0	9	21	AAB12006	Brain homing pepti
99	3	60.0	9	21	AAV96352	HLA-A3 binding pep
100	3	60.0	9	21	AAV86697	Telomerase peptide

#### ALIGNMENTS

RESULT 1  
AAP71643



ID AAP71643 standard; Protein; 5 AA.  
 XX  
 AC AAP71643;  
 XX  
 DT 07-MAY-1991 (first entry)  
 XX  
 DE Diuretic peptide deriv.  
 XX  
 KW Diuretic; natriuretic; kaliuretic; urine; sodium; potassium;  
 KW excretion.  
 XX  
 OS synthetic.  
 XX  
 PN EP249169-A.  
 XX  
 PD 16-DEC-1987.  
 XX  
 PF 05-JUN-1987; 87EP-0108184.  
 XX  
 PR 11-JUN-1986; 86DE-3619633.  
 XX  
 PA (FARH ) HOECHST AG.  
 XX  
 PI Konig W, Breipohl G, Geiger R, Knolle J, Hropot M;  
 XX  
 DR WPI; 1987-349887/50.  
 XX  
 PT New peptide derivs. - affecting urine, sodium and/or potassium  
 PT excretion  
 XX  
 PS Example 16; page 19; 35pp; German.  
 XX  
 CC This peptide deriv. has diuretic, natriuretic and kaliuretic  
 CC activities. It affects urine, sodium and/or potassium secretion.  
 CC Val(2) is D-Val.  
 CC See also AAP71636, AAP71638-42 and AAP71644-55.  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 2 VLR 4

#### RESULT 2

AAR67200

ID AAR67200 standard; peptide; 5 AA.  
 XX  
 AC AAR67200;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 02-AUG-1995 (first entry)  
 XX

DE Bovine glial cell growth factor-2 (GGF-2) peptide fragment.  
 XX  
 KW Glial cell growth factor-2; GGF-2; mammalian muscle cell treatment;  
 KW skeletal; cardiac; smooth; acetylcholine receptor deficiency.  
 XX  
 OS Bos taurus.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /note= "unknown"  
 XX  
 PN WO9426298-A1.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 06-MAY-1994; 94WO-US05083.  
 XX  
 PR 06-MAY-1993; 93US-0059022.  
 PR 08-MAR-1994; 94US-0209204.  
 XX  
 PA (CAMB-) CAMBRIDGE NEUROSCIENCE.  
 XX  
 PI Gwynne DI, Marchionni M, Sklar R;  
 XX  
 DR WPI; 1995-006353/01.  
 XX  
 PT Treating mammalian muscle diseases and disorders - by admin. of  
 PT GGF2 and other specified polypeptide(s) which bind the p185erbB2  
 PT receptor.  
 XX  
 PS Example 9; Page 154; 241pp; English.  
 XX  
 CC AAR67165-R67173 and AAR67199-R67201 are bovine glial cell growth  
 CC factor-2 (GGF-2) peptide fragments. A 55-63kD polypeptide factor  
 CC known to have glial cell mitogenic activity, which includes one  
 CC of the above peptide fragments in its amino acid sequence is  
 CC claimed. The polypeptide can be used to treat a variety of  
 CC mammalian skeletal, cardiac and smooth muscle diseases,  
 CC including acetylcholine receptor deficiency.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 16; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 3 VLR 5

RESULT 3  
 AAW09683  
 ID AAW09683 standard; peptide; 5 AA.  
 XX  
 AC AAW09683;

XX  
DT 23-MAY-1997 (first entry)  
XX  
DE Cyclic pentapeptide having thrombolytic activity.  
XX  
KW thrombolysis; arteriosclerosis; cyclic.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "this residue forms part of a cyclic  
FT peptide, being condensed with the amino acid  
FT at position 5. It is not an N-terminal site"  
FT Modified-site 5  
FT /note= "this residue forms part of a cyclic  
FT peptide, being condensed with the amino acid  
FT at position 1. It is not a C-terminal site"  
FT Misc-difference 1  
FT /note= "D-form residue"  
FT Misc-difference 3  
FT /note= "D-form residue"  
FT Misc-difference 5  
FT /note= "D-form residue"  
XX  
PN JP08217794-A.  
XX  
PD 27-AUG-1996.  
XX  
PF 15-FEB-1995; 95JP-0026674.  
XX  
PR 15-FEB-1995; 95JP-0026674.  
XX  
PA (BIOC-) BIOCOSMOS YG.  
XX  
DR WPI; 1996-439571/44.  
XX  
PT New cyclic penta:peptide - exhibits thrombolytic and  
PT anti-arteriosclerosis activity  
XX  
PS Disclosure; Page 8; 9pp; Japanese.  
XX  
CC The invention relates to new cyclic pentapeptides of formula  
CC cyclo(A-B-C-D-E) in which A is Val, Leu, Phe, Lys, Arg, Glu, Gln or  
CC Ser; B is Leu, Val, Phe, Lys, Arg, His, Glu, Gln, Ala or Ser; C is Leu,  
CC Val, alle, Phe, Lys, Arg, Glu, Gln, Ala or Ser; D is Phe, Val, Leu, Tyr,  
CC Lys, arg, His, Glu, Gln, Ala or Ser; and E is Arg, Val, Leu, Phe, Lys,  
CC His, Glu, Asn, Ala or Ser. The amino acids may be in D- or L-form.  
CC The peptides have thrombolytic activity and anti-arteriosclerotic  
CC activity.  
CC The present sequence is a specific example of the new peptides.  
XX  
SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 17; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2	VLR	4
Db	1	VLR	3

# RESULT 4

AAR86664

ID AAR86664 standard; peptide; 5 AA.

XX

AC AAR86664;

XX

DT 03-JUL-1996 (first entry)

XX

DE GGF II tryptic peptide GGF-II 06.

XX

KW Glial growth factor; GGF; human; hGGF2; Schwann cell; mitogenesis; GGF-I;  
 KW glial cell; therapy; peripheral nerve damage; demyelination; bovine;  
 KW glial tumour; fibroblast proliferation; wound repair; multiple sclerosis;  
 KW neurodegenerative disorder; neural regeneration; acetylcholine receptor;  
 KW GGF-II.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /label= Lys, Arg

XX

PN W09532724-A1.

XX

PD 07-DEC-1995.

XX

PF 25-MAY-1995; 95WO-US06846.

XX

PR 26-MAY-1994; 94US-0249322.

XX

PA (CAMB-) CAMBRIDGE NEUROSCIENCE.

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Chen MS, Goodearl AD, Hiles I, Marchionni M, Minghetti L;

PI Stroobant P, Waterfield M;

XX

DR WPI; 1996-030329/03.

XX

PT Glial growth factors with Schwann cell mitogenic activity - for  
 PT prophylaxis or treatment of nerve disorders, e.g. Multiple Sclerosis

XX

PS Example 2; Fig 11; 199pp; English.

XX

CC AAR86659-R86677 represent fragments of bovine glial growth factor II  
 CC (GGF-II). These fragments were obtained by lysyl endopeptidase and  
 CC protease V8 digests. These sequences have Schwann cell mitogenic  
 CC activity in the presence of foetal calf plasma. These sequences, GGF-I  
 CC peptide sequences (see AAR86629-R86657), and human GGF2 (see AAR86628)  
 CC are used to stimulate mitogenesis of glial cells, for prophylaxis or  
 CC treatment of a pathophysiological condition of the nervous system in a  
 CC mammal. Also, for identification of a receptor, for treatment of

CC conditions of peripheral nerve damage (e.g. demyelination/damage/loss of  
CC Schwann cells), treatment of neurodegenerative disorders in mammals, for  
CC inducing neural regeneration, fibroblast proliferation or wound repair.  
CC Glial tumours can be treated by inhibiting this sequence binding to its  
CC receptor. These peptides are also able to induce synthesis of  
CC acetylcholine receptor, and is useful in prophylaxis or treatment of  
CC multiple sclerosis in a patient.

XX

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 17; Length 5;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4

|||

Db 3 VLR 5

#### RESULT 5

AAW13413

ID AAW13413 standard; Peptide; 5 AA.

XX

AC AAW13413;

XX

DT 15-JAN-1998 (first entry)

XX

DE Brain homing peptide generic sequence.

XX

KW Brain homing peptide; in vivo panning; screening; phage display;  
KW drug delivery.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "Xaa at position 1 is absent or is about  
FT 1-10 independently selected amino acids"

FT Misc-difference 5

FT /note= "Xaa at position 5 is about 1-20  
FT idenpendently selected amino acids"

XX

PN WO9710507-A1.

XX

PD 20-MAR-1997.

XX

PF 10-SEP-1996; 96WO-US14600.

XX

PR 11-SEP-1995; 95US-0526710.

PR 11-SEP-1995; 95US-0526708.

XX

PA (LJOL-) LA JOLLA CANCER RES FOUND.

XX

PI Pasqualini R, Ruoslahti E;

XX

DR WPI; 1997-202359/18.

XX

PT Obtaining compound that homes to selected organ or tissue - by in  
PT vivo panning method, specifically to identify brain, kidney,  
PT angiogenic vasculature or tumour tissue homing peptide(s)  
XX  
PS Claim 12; Page 67; 75pp; English.  
XX  
CC This synthetic generic peptide is a claimed example of a brain-  
CC homing peptide that was identified using a novel method for  
CC obtaining molecules that home to a selected organ or tissue. This  
CC in vivo panning method typically involves administering a phage  
CC display library to a subject, and identifying expressed peptides  
CC which home to the desired organ or tissue, e.g. brain, kidney,  
CC angiogenic vascular or tumour tissue. The isolated peptides (see  
CC AAW13412-52, AAW11181-86) can be used to target e.g. drugs, toxins or  
CC labels to the selected organ/tissue (claimed) or to identify and/or  
CC isolate target molecules (claimed). The peptides can be directly  
CC identified in vivo, as compared to prior art in vitro screening  
CC methods, which require further examination to see if they maintain  
CC specificity in vivo.  
XX  
SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 18; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
| | |  
Db 2 VLR 4

RESULT 6  
AAW51298  
ID AAW51298 standard; peptide; 5 AA.  
XX  
AC AAW51298;  
XX  
DT 15-SEP-1998 (first entry)  
XX  
DE Human B-type natriuretic peptide variant, C-terminal sequence.  
XX  
KW B-type natriuretic peptide; clearance receptor; electrolyte balance;  
KW diuretic; vasodilator; circulation; natriuresis; diuresis; hNPR-C;  
KW cyclic guanosine monophosphate; cGMP; second messenger; variant.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1  
FT /label= Asn, Lys  
FT Misc-difference 5  
FT /label= Arg, Lys  
XX  
PN WO9817690-A1.  
XX  
PD 30-APR-1998.  
XX

PF 09-OCT-1997; 97WO-US18384.  
 XX  
 PR 22-OCT-1996; 96US-0731880.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Lowe DG, Schoenfeld JR;  
 XX  
 DR WPI; 1998-261429/23.  
 XX  
 PT Variants of brain natriuretic peptide with reduced affinity for  
 PT clearance receptor - for treating disorders of electrolyte balance  
 PT and as diuretics and vasodilators, have increased circulation time  
 PT and in vivo activity  
 XX  
 PS Disclosure; Page 8; 55pp; English.  
 XX  
 CC The invention relates to variants of brain natriuretic peptide (BNP)  
 CC with reduced affinity for the human clearance receptor (hNPR-C) relative  
 CC to wild-type BNP. The variants are used: (a) to treat or prevent  
 CC disorders of electrolyte balance, or (b) to induce natriuresis, diuresis  
 CC or vasodilation. Typical applications are in congestive heart failure,  
 CC arrhythmia, hypertension, nephrotic syndrome, pre-eclampsia, premenstrual  
 CC syndrome, hepatic cirrhosis, pulmonary disease and renal failure  
 CC (associated with inefficient renal perfusion or reduced glomerular  
 CC filtration rate). The variants are also useful as intermediates and as  
 CC modulators of other compounds with similar activities. Although the  
 CC variants have reduced affinity for NPR-C, they have at least equal  
 CC affinity for the A receptor (NPR-A) and ability to stimulate cyclic  
 CC guanosine monophosphate (cGMP), second messenger, production. The  
 CC variants should persist for longer in the circulation and thus have  
 CC greater in vivo activity. The present sequence represents the  
 CC C-terminal sequence of a BNP variant.  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 2 VLR 4

# RESULT 7

AAW97427

ID AAW97427 standard; peptide; 5 AA.

XX

AC AAW97427;

XX

DT 19-MAY-1999 (first entry)

XX

DE Shigella-like toxin epitope from Escherichia coli O157:H7.

XX

KW Shigella-like toxin; SLT; Escherichia coli O157:H7;

KW epitope; vaccine.

XX  
 OS Escherichia coli.  
 XX  
 PN WO9905169-A1.  
 XX  
 PD 04-FEB-1999.  
 XX  
 PF 17-JUL-1998; 98WO-GB02156.  
 XX  
 PR 21-JUL-1997; 97GB-0015177.  
 XX  
 PA (NEUT-) NEUTEC PHARMA PLC.  
 XX  
 PI Burnie JP, Matthews RC;  
 XX  
 DR WPI; 1999-142851/12.  
 XX  
 PT New epitopes of shigella-like toxin (SLT) - useful in the diagnosis  
 PT and treatment of pathogens expressing SLTs, particularly E. coli  
 PT 0157:H7  
 XX  
 PS Claim 1; Page 21; 29pp; English.  
 XX  
 CC AAW97424-30 represents epitope of shigella-like toxin (SLT) from  
 CC Escherichia coli 0157:H7. The epitopes and their binding agents  
 CC are used in the diagnosis and treatment of animals or humans.  
 CC The epitopes can be used as an immunogen or vaccine.  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 3 VLR 5

# RESULT 8

AAAY80232

ID AAY80232 standard; peptide; 5 AA.

XX

AC AAY80232;

XX

DT 25-MAY-2000 (first entry)

XX

DE B-type natriuretic peptide variant C-terminal peptide SEQ ID NO:41.

XX

KW Human; B-type natriuretic peptide; BNP; clearance receptor; diuretic;  
 KW water imbalance; electrolyte imbalance; natriuretic peptide receptor;  
 KW natriuresis; diuresis; vasodilation; hypotensive; cardiatic; hepatotropic;  
 KW nephrotropic; vasorelaxant; hypertension; congestive heart failure;  
 KW nephrotic syndrome; hepatic cirrhosis; pulmonary disease; renal failure.

XX

OS Mammalia.

XX



FH Key Location/Qualifiers  
 FT Misc-difference 1  
 FT /label= Asn, Lys  
 FT Misc-difference 5  
 FT /label= Arg, Lys  
 XX  
 PN US6028055-A.  
 XX  
 PD 22-FEB-2000.  
 XX  
 PF 21-OCT-1997; 97US-0954915.  
 XX  
 PR 22-OCT-1996; 96US-0028854.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Schoenfeld JR, Lowe DG;  
 XX  
 DR WPI; 2000-194846/17.  
 XX  
 PT B-type natriuretic peptide (BNP) variant (I) having a decreased binding  
 PT affinity for the human clearance receptor, useful for treating  
 PT natriuresis, diuresis or vasodilation -  
 XX  
 PS Disclosure; Column 8; 33pp; English.  
 XX  
 CC The present invention describes a B-type natriuretic peptide (BNP)  
 CC variant (I) having a decreased binding affinity for the human clearance  
 CC receptor compared to human wild-type BNP. The present invention also  
 CC describes a method for treating a disorder of electrolyte balance  
 CC including natriuresis, diuresis or vasodilation comprising administering  
 CC a composition comprising (I). (I) has hypotensive, cardiant,  
 CC hepatotropic, nephrotropic, natriuretic, diuretic and vasorelaxant  
 CC activities. (I) can be used for the treatment or prophylaxis of  
 CC conditions associated with water or electrolyte imbalance and  
 CC hypertension, such as congestive heart failure (CHF), nephrotic syndrome  
 CC and hepatic cirrhosis, pulmonary disease, and renal failure due to  
 CC ineffective renal perfusion or reduced glomerular filtration rate. (I)  
 CC can also useful for treating natriuresis, diuresis or vasodilation.  
 CC The present sequence represents an C-terminal peptide from a BNP  
 CC variant given in the present invention.  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
 |||  
 Db 2 VLR 4

RESULT 9  
 AAY68290  
 ID AAY68290 standard; Peptide; 5 AA.  
 XX

AC AAY68290;  
 XX  
 DT 13-APR-2000 (first entry)  
 XX  
 DE Peptide SEQ ID NO:122.  
 XX  
 KW MHC class I; major histocompatibility complex; microglobulin; antigen;  
 KW immune response; immunisation; AIDS; multiple sclerosis; toxic shock;  
 KW cancer; lupus erythematosus; snake bite; cytostatic; antiviral;  
 KW immunomodulatory; dermatological; immunosuppressive; antiinflammatory;  
 KW neuroprotective.  
 XX  
 OS Unidentified.  
 XX  
 PN US6011146-A.  
 XX  
 PD 04-JAN-2000.  
 XX  
 PF 07-JUN-1995; 95US-0481985.  
 XX  
 PR 15-NOV-1991; 91US-0792473.  
 PR 05-DEC-1991; 91US-0801818.  
 XX  
 PA (INSP ) INST PASTEUR.  
 PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
 XX  
 PI Kourilsky P, Mottez E, Abastado J;  
 XX  
 DR WPI; 2000-125951/11.  
 XX  
 PT New recombinant DNA encoding covalently linked form of major  
 PT histocompatibility complex Class I determinant, used for immune system  
 PT stimulation, e.g. for treating cancer -  
 XX  
 PS Disclosure; Column 149; 88pp; English.  
 XX  
 CC The present invention describes a recombinant DNA molecule (I)  
 CC containing a sequence (Ia) that encodes an altered MHC (major  
 CC histocompatibility complex ) Class I determinant (II) comprises a  
 CC polypeptide with alpha1, alpha2, alpha3 and beta2-microglobulin  
 CC domains, in which alpha3 and beta2 are covalently linked, thorough C-  
 CC and N-termini respectively, via a nucleotide spacer sequence encoding a  
 CC polypeptide. (II) includes an antigen-binding site and when (II) and  
 CC the antigen are associated they are recognized by a mammalian T cell  
 CC receptor (TCR). (I) are used to produce (II) which are used to study  
 CC functional interactions between the various MHC domains. They can also  
 CC be used to modulate (in vivo or in vitro) the immune system by inducing  
 CC an effector response (cytotoxicity, antibody synthesis, phagocytosis)  
 CC of immune system cells, typically for treating, or immunising against;  
 CC cancer, acquired immune deficiency syndrome, lupus erythematosus,  
 CC multiple sclerosis, toxic shock and snake bite, but also for selective  
 CC destruction of autoreactive cells, diagnostically to assay T cell  
 CC receptors and to raise specific antibodies (useful for diagnosis,  
 CC therapy, studying MHC-associated cellular processes and for affinity  
 CC purification). AAZ57558 and AAY68186 to AAY68316 are sequences used in  
 CC the exemplification of the present invention.  
 XX

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 1 VLR 3

RESULT 10

AA52944

ID AA52944 standard; Peptide; 5 AA.

XX

AC AA52944;

XX

DT 14-FEB-2000 (first entry)

XX

DE MHC domain DR peptide SEQ ID NO:122.

XX

KW Major histocompatibility complex; MHC class I; MHC class II; antigen;  
KW immune response; diagnosis; antibody; immunisation; autoimmune disease;  
KW acquired immune deficiency syndrome; AIDS; cytostatic; dermatological;  
KW anti-inflammatory; neuroprotective; immunosuppressive; antithyroid;  
KW vaccine; lupus erythematosus; multiple sclerosis; thyroiditis;  
KW toxic shock; tumour; snakebite.

XX

OS Mammalia.

XX

PN US5976551-A.

XX

PD 02-NOV-1999.

XX

PF 07-JUN-1995; 95US-0484905.

XX

PR 05-DEC-1991; 91US-0801818.

PR 15-NOV-1991; 91US-0792473.

XX

PA (INSP ) INST PASTEUR.

PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

XX

PI Kourilsky P, Mottez E, Abastado J;

XX

DR WPI; 2000-037081/03.

XX

PT Composition containing an antigen and altered major histocompatibility  
PT Class II determinant, used to immunize against autoimmune diseases,  
PT e.g. acquired immune deficiency syndrome -

XX

PS Disclosure; Column 173; 96pp; English.

XX

CC The present invention describes a composition capable of eliciting  
CC anti-major histocompatibility (MHC) antibodies. The composition  
CC comprises an antigen associated with an altered MHC Class II determinant  
CC (I) comprising alpha1, alpha2, beta1 and beta2 polypeptide domains  
CC encoded by a mammalian MHC Class II locus covalently linked to form a

CC polypeptide (I) containing beta2, alpha2, alpha1 and beta1 domains in  
 CC sequence. The resulting Antigen-MHC complex is recognizable by the T cell  
 CC receptor. The compositions are used for immunisation against, or  
 CC treatment of, a wide range of autoimmune diseases, e.g. acquired immune  
 CC deficiency syndrome (AIDS), lupus erythematosus, multiple sclerosis,  
 CC thyroiditis, toxic shock, tumour and snakebite, depending on the nature  
 CC of antigen. (I) is also used to analyse functional interactions between  
 CC the various domains and for targeting lymphocyte receptors. Antibodies  
 CC against (I) are produced by usual methods of immunisation or cell fusion,  
 CC and may be humanised by standard methods. These antibodies are useful for  
 CC diagnosis (detection or purification of MHC gene products), therapy  
 CC (neutralising MHC on cell surfaces) and in the study of MHC and cellular  
 CC processes. AAZ33240 to AAZ33242 and AAY52840 to AAY52970 represent  
 CC sequences used in the exemplification of the present invention.

XX

SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 1 VLR 3

# RESULT 11

AAU03880

ID AAU03880 standard; Peptide; 5 AA.

XX

AC AAU03880;

XX

DT 12-SEP-2001 (first entry)

XX

DE G protein-coupled receptor-like (GPCR-like) receptor binding peptide #50.

XX

KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
 KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
 KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;  
 KW fruitfly.

XX

OS Synthetic.

XX

PN WO200138533-A2.

XX

PD 31-MAY-2001.

XX

PF 24-NOV-2000; 2000WO-US32225.

XX

PR 24-NOV-1999; 99US-0167523.

XX

PA (PHAA ) PHARMACIA & UPJOHN.

XX

PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;

XX

DR WPI; 2001-343952/36.

XX

PT Using G-protein-coupled receptor (GPCR)-like receptors to identify  
PT candidate compounds for the treatment and prevention of invertebrate  
PT parasites, especially helminths and insects -  
XX  
PS Claim 14; Page 56; 219pp; English.  
XX  
CC The sequence represents a G protein-coupled receptor-like (GPCR-like)  
CC receptor protein. GPCR-like receptors and their associated nucleic acids  
CC may be used to identify candidate compounds for their ability to modulate  
CC the activity of GPCRs. The sequences therefore are useful for treating  
CC and preventing infection by endoparasitic and ectoparasitic invertebrate  
CC parasites, especially helminths and insects, and particularly ailments  
CC related to aberrant neurological and neuromuscular function.  
XX  
SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

# RESULT 12

AAU03881

ID AAU03881 standard; Peptide; 5 AA.

XX

AC AAU03881;

XX

DT 12-SEP-2001 (first entry)

XX

DE G protein-coupled receptor-like (GPCR-like) receptor binding peptide #51.

XX

KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;  
KW fruitfly.

XX

OS Synthetic.

XX

PN WO200138533-A2.

XX

PD 31-MAY-2001.

XX

PF 24-NOV-2000; 2000WO-US32225.

XX

PR 24-NOV-1999; 99US-0167523.

XX

PA (PHAA ) PHARMACIA & UPJOHN.

XX

PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;

XX

DR WPI; 2001-343952/36.

XX

PT Using G-protein-coupled receptor (GPCR)-like receptors to identify

PT candidate compounds for the treatment and prevention of invertebrate  
PT parasites, especially helminths and insects -  
XX  
PS Claim 14; Page 56; 219pp; English.  
XX  
CC The sequence represents a G protein-coupled receptor-like (GPCR-like)  
CC receptor protein. GPCR-like receptors and their associated nucleic acids  
CC may be used to identify candidate compounds for their ability to modulate  
CC the activity of GPCRs. The sequences therefore are useful for treating  
CC and preventing infection by endoparasitic and ectoparasitic invertebrate  
CC parasites, especially helminths and insects, and particularly ailments  
CC related to aberrant neurological and neuromuscular function.  
XX  
SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

# RESULT 13

AAB58705

ID AAB58705 standard; peptide; 5 AA.

XX

AC AAB58705;

XX

DT 13-MAR-2001 (first entry)

XX

DE Altered MHC determinant peptide #2.

XX

KW Major histocompatibility complex; MHC class I; immune; snake bite;

KW T cell mediated autoimmune disease; AIDS; lupus erythematosus;

KW toxic shock.

XX

OS Unidentified.

XX

PN US6153408-A.

XX

PD 28-NOV-2000.

XX

PF 09-JAN-1995; 95US-0370476.

XX

PR 15-NOV-1991; 91US-0792473.

PR 07-SEP-1993; 93US-0117575.

PR 05-DEC-1991; 91US-0801818.

PR 07-JUN-1993; 93US-0072787.

XX

PA (INSP ) INST PASTEUR.

PA (INRM ) INST NAT SANTE & RECH MEDICAL.

XX

PI Abastado J, Kourilsky P, Casrouge A, Ojcius D, Lone Y, Mottez E;

XX

DR WPI; 2001-060089/07.

XX  
PT New altered major histocompatibility complex (MHC) class I determinant  
PT useful for eliciting an immune response and/or for immunizing against  
PT or treating diseases, for example, multiple sclerosis, AIDS, toxic  
PT shock or snake bite -

XX  
PS Disclosure; Column 163; 105pp; English.

XX  
CC The present invention relates to a major histocompatibility complex  
CC (MHC) class I determinant, which has alpha\_1 alpha\_2 alpha\_3 and  
CC beta2-microglobulin polypeptide domains encoded by a mammalian MHC  
CC class I locus. The MHC class I determinants are useful for activating  
CC the immune system and presenting antigens to the immune system to  
CC elicit an antigenic response. The MHC class I determinants are also  
CC useful for treating diseases, e.g. T cell mediated autoimmune disease,  
CC AIDS, lupus erythematosus, toxic shock or snake bite. The altered MHC  
CC class I determinants and compositions containing antigens bound to  
CC the determinants are useful in diagnostic applications, e.g. altered  
CC determinants may be used to target lymphocyte receptors and the  
CC resulting bound determinant can be assayed.

XX  
SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 1 VLR 3

#### RESULT 14

AAO19570

ID AAO19570 standard; Peptide; 5 AA.

XX

AC AAO19570;

XX

DT 28-JAN-2003 (first entry)

XX

DE M sterilia protein fragment #5.

XX

KW Substance PF1022; biosynthesis; transgenic; chorismic acid; anthelmintic;  
KW phenylalanine; p-aminophenylpyruvic acid; pharmaceutical;  
KW veterinary drug.

XX

OS Mycelia sterilia.

XX

PN WO200277244-A1.

XX

PD 03-OCT-2002.

XX

PF 22-MAR-2002; 2002WO-JP02782.

XX

PR 22-MAR-2001; 2001JP-0082227.

XX

PA (MEIJ ) MEIJI SEIKA KAISHA LTD.

XX  
 PI Yanai K, Sumida N, Watanabe M, Moriya T, Murakami T;  
 XX  
 DR WPI; 2003-018934/01.  
 XX  
 PT Novel biosynthesis gene-transferred transformants for producing PF1022  
 PT substance derivatives by fermentation, as pharmaceuticals or veterinary  
 PT drugs with anthelmintic activity -  
 XX  
 PS Example 13; Page 105; 116pp; Japanese.  
 XX  
 CC The present invention relates to transformants capable of producing  
 CC PF1022 substance derivatives. These were obtained by transferring a gene  
 CC participating in the biosynthesis pathway from chorismic acid to  
 CC p-aminophenylpyruvic acid (biosynthesis gene) into a  
 CC phenylalanine-requiring host derived from an organism producing the  
 CC PF1022 substance. The transformants are producing PF1022 substance  
 CC derivatives by fermentation, for use as pharmaceuticals or veterinary  
 CC drugs. The present sequence is a fragment of a Mycelia sterilia protein  
 CC described in the exemplification of the invention.  
 XX  
 SQ Sequence 5 AA;

Query Match 60.0%; Score 3; DB 24; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 3 VLR 5

# RESULT 15

AAW51290

ID AAW51290 standard; peptide; 6 AA.  
 XX  
 AC AAW51290;  
 XX  
 DT 15-SEP-1998 (first entry)  
 XX  
 DE Human B-type natriuretic peptide variant partial sequence.  
 XX  
 KW B-type natriuretic peptide; clearance receptor; electrolyte balance;  
 KW diuretic; vasodilator; circulation; natriuresis; diuresis; hNPR-C;  
 KW cyclic guanosine monophosphate; cGMP; second messenger; variant.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9817690-A1.  
 XX  
 PD 30-APR-1998.  
 XX  
 PF 09-OCT-1997; 97WO-US18384.  
 XX  
 PR 22-OCT-1996; 96US-0731880.  
 XX  
 PA (GETH ) GENENTECH INC.



XX  
 PI Lowe DG, Schoenfeld JR;  
 XX  
 DR WPI; 1998-261429/23.  
 XX  
 PT Variants of brain natriuretic peptide with reduced affinity for  
 PT clearance receptor - for treating disorders of electrolyte balance  
 PT and as diuretics and vasodilators, have increased circulation time  
 PT and in vivo activity  
 XX  
 PS Claim 7; Page 46; 55pp; English.  
 XX  
 CC The invention relates to variants of brain natriuretic peptide (BNP)  
 CC with reduced affinity for the human clearance receptor (hNPR-C) relative  
 CC to wild-type BNP. The variants are used: (a) to treat or prevent  
 CC disorders of electrolyte balance, or (b) to induce natriuresis, diuresis  
 CC or vasodilation. Typical applications are in congestive heart failure,  
 CC arrhythmia, hypertension, nephrotic syndrome, pre-eclampsia, premenstrual  
 CC syndrome, hepatic cirrhosis, pulmonary disease and renal failure  
 CC (associated with inefficient renal perfusion or reduced glomerular  
 CC filtration rate). The variants are also useful as intermediates and as  
 CC modulators of other compounds with similar activities. Although the  
 CC variants have reduced affinity for NPR-C, they have at least equal  
 CC affinity for the A receptor (NPR-A) and ability to stimulate cyclic  
 CC guanosine monophosphate (cGMP), second messenger, production. The  
 CC variants should persist for longer in the circulation and thus have  
 CC greater in vivo activity. The present sequence represents a BNP  
 CC variant partial sequence.  
 XX  
 SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 19; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 2 VLR 4

# RESULT 16

AAW56842

ID AAW56842 standard; peptide; 6 AA.

XX

AC AAW56842;

XX

DT 28-JUL-1998 (first entry)

XX

DE Enzyme inhibitor peptide SEQ ID NO:43.

XX

KW Enzyme inhibitor; t-PA; u-PA; chymotrypsin; serine protease; active;

KW latent; substrate subtraction phage display peptide library;

KW identification; kinase; phosphatase; serpin.

XX

OS Homo sapiens.

XX

PN WO9747314-A1.

XX  
PD 18-DEC-1997.  
XX  
PF 10-JUN-1997; 97WO-US09760.  
XX  
PR 10-JUN-1996; 96US-0019495.  
XX  
PA (SCRI ) SCRIPPS RES INST.  
XX  
PI Ke S, Madison EL;  
XX  
DR WPI; 1998-062746/06.  
XX  
PT Substrate subtraction phage display peptide libraries - used to  
PT distinguish between active and latent forms of enzyme, e.g. serine  
PT protease  
XX  
PS Claim 25; Page 54; 138pp; English.  
XX  
CC The present sequence represents an enzyme inhibitor peptide used in  
CC the method of the invention to distinguish between t-PA and u-PA. The  
CC present invention describes a substrate subtraction library for the  
CC identification of peptide substrates selective between a first enzyme  
CC (E1) and a second enzyme (E2), comprising a collection different  
CC peptides, substantially lacking peptides that are effective substrates  
CC for E1. Also described are: (1) a method (M1) for identifying peptide  
CC substrates selective between a first enzyme (E1) and a second enzyme  
CC (E2); (2) a compound comprising the amino acid sequence of a peptide  
CC identified by M1; (3) a polypeptide for use as an enzyme inhibitor  
CC comprising one of 237 amino acid sequences (see AAW56801 to AAW56947,  
CC and AAW56949 to AAW57038); (4) a recombinant DNA vector comprising DNA  
CC (I) encoding a protease inhibitor including the sequence identified by  
CC the M1; (5) a prokaryotic or eukaryotic cell containing the vector of  
CC (4); (6) an antibody (Ab) immunoreactive with at least one of the  
CC peptides identified by M1; and (7) a diagnostic assay for distinguishing  
CC between active and latent forms of protease inhibitors, that uses (Ab).  
CC The library and method are used for distinguishing between active and  
CC latent forms of enzyme inhibitors, e.g. proteases, kinases and  
CC phosphatases. (Ab) are used for affinity purification of recombinant  
CC peptides and in the identification of naturally occurring protease  
CC inhibitors. Enzyme- inhibiting peptides identified can be used to treat a  
CC serpin deficiency or a disorder of serine proteases.  
XX  
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 19; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 17  
AAV55285  
ID AAV55285 standard; peptide; 6 AA.

XX  
 AC AAY55285;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE ATCC HB 11885 monoclonal antibody 9079 releasing peptide SEQ ID NO:179.  
 XX  
 KW Antibody releasing peptide; CD34; hybridoma; binding; antigen;  
 KW cell surface antigen; identification; haematopoietic stem cell;  
 KW tumour; cancer; immune system; therapy; displacement.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5968753-A.  
 XX  
 PD 19-OCT-1999.  
 XX  
 PF 07-JUN-1995; 95US-0482228.  
 XX  
 PR 14-JUN-1994; 94US-0259427.  
 XX  
 PA (NEXE-) NEXELL THERAPEUTICS INC.  
 XX  
 PI Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;  
 PI Al-Abdaly FA;  
 XX  
 DR WPI; 1999-590399/50.  
 XX  
 PT Short peptides useful for displacing antibodies from cell surface  
 PT antigens. -  
 XX  
 PS Example 9; Column 33; 81pp; English.  
 XX  
 CC The present invention describes peptides of 4-17 amino acids which  
 CC displace either the anti-CD34 monoclonal antibody designated 561, the  
 CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC  
 CC HB-11646 (designated 9069), the anti-CD34 antibody produced by  
 CC hybridoma ATCC HB-11885 (9079), or the anti-human breast cancer  
 CC antibody produced by hybridoma ATCC HB-11884 (9187), from a cell  
 CC surface antigen on a target cell. The peptides are useful for  
 CC displacing antibodies bound to cell surfaces to release cells that  
 CC have been positively selected by antibody-mediated binding to beads  
 CC or other solid support. AAY55107 to AAY55319 represent peptides used in  
 CC the exemplification of the present invention.  
 XX  
 SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 2 VLR 4

RESULT 18

AAY80220

ID AAY80220 standard; peptide; 6 AA.

XX

AC AAY80220;

XX

DT 25-MAY-2000 (first entry)

XX

DE Human B-type natriuretic peptide variant formula I C-terminal peptide.

XX

KW Human; B-type natriuretic peptide; BNP; clearance receptor; diuretic;  
KW water imbalance; electrolyte imbalance; natriuretic peptide receptor;  
KW natriuresis; diuresis; vasodilation; hypotensive; cardiant; hepatotropic;  
KW nephrotropic; vasorelaxant; hypertension; congestive heart failure;  
KW nephrotic syndrome; hepatic cirrhosis; pulmonary disease; renal failure.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN US6028055-A.

XX

PD 22-FEB-2000.

XX

PF 21-OCT-1997; 97US-0954915.

XX

PR 22-OCT-1996; 96US-0028854.

XX

PA (GETH ) GENENTECH INC.

XX

PI Schoenfeld JR, Lowe DG;

XX

DR WPI; 2000-194846/17.

XX

PT B-type natriuretic peptide (BNP) variant (I) having a decreased binding  
PT affinity for the human clearance receptor, useful for treating  
PT natriuresis, diuresis or vasodilation -

XX

PS Disclosure; Column 3; 33pp; English.

XX

CC The present invention describes a B-type natriuretic peptide (BNP)  
CC variant (I) having a decreased binding affinity for the human clearance  
CC receptor compared to human wild-type BNP. The present invention also  
CC describes a method for treating a disorder of electrolyte balance  
CC including natriuresis, diuresis or vasodilation comprising administering  
CC a composition comprising (I). (I) has hypotensive, cardiant,  
CC hepatotropic, nephrotropic, natriuretic, diuretic and vasorelaxant  
CC activities. (I) can be used for the treatment or prophylaxis of  
CC conditions associated with water or electrolyte imbalance and  
CC hypertension, such as congestive heart failure (CHF), nephrotic syndrome  
CC and hepatic cirrhosis, pulmonary disease, and renal failure due to  
CC ineffective renal perfusion or reduced glomerular filtration rate. (I)  
CC can also useful for treating natriuresis, diuresis or vasodilation.  
CC The present sequence represents an C-terminal peptide option in the  
CC BNP variant formula from the present invention.

XX

SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 19

AAAY87031

ID AAY87031 standard; Peptide; 6 AA.

XX

AC AAY87031;

XX

DT 09-MAY-2000 (first entry)

XX

DE Human haematopoietic CD34+ cell binding peptide SEQ ID #179.

XX

KW Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody;

KW non-enzymatic cell selection method; haematopoietic stem cell;

KW haematopoietic progenitor cell; antibody 561; breast cancer cell;

KW antibody 9187; cell surface determinant; diagnostic cell based assay.

XX

OS Homo sapiens.

XX

PN US6017719-A.

XX

PD 25-JAN-2000.

XX

PF 07-JUN-1995; 95US-0482528.

XX

PR 14-JUN-1994; 94US-0259427.

XX

PA (NEXE-) NEXELL THERAPEUTICS INC.

XX

PI Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;

PI Al-Abdaly FA;

XX

DR WPI; 2000-136676/12.

XX

PT Non-enzymatic method for the positive selection of target cells from a  
PT heterogeneous cell suspension, useful for selecting human breast cancer  
PT cells from a patient's blood or bone marrow -

XX

PS Example 9; Column 38; 82pp; English.

XX

CC This sequence represents a human haematopoietic CD34+ cell binding  
CC peptide, and was used to test the method of the invention. The method is  
CC a non-enzymatic method for the positive selection of one or more target  
CC cells from a heterogeneous cell suspension, by using specific peptides  
CC which effect the displacement and release of a specific target cell  
CC from a specific monoclonal antibody. The method is useful for positive  
CC selection and specific release of target human haematopoietic  
CC stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and  
CC the antibody 561. The method is also useful for positive selection and  
CC specific release of target human breast cancer cells, bound by the

CC monoclonal anti-breast cancer antibody 9187, from a patient's blood or  
CC bone marrow. Identification of peptide epitopes for antibodies which  
CC recognise cell surface determinants also allows construction of  
CC diagnostic cell based assays. The peptide mediated release is enzyme free  
CC and thus leaves the cell surface proteins intact. Moreover, peptide  
CC mediated release leaves the target cell free of bound antibody or  
CC antibody fragments. The method also produces a high yield of functional  
CC target cells and is relatively inexpensive to carry out.

XX

SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4

|||

Db 2 VLR 4

#### RESULT 20

ABM00062

ID ABM00062 standard; Peptide; 6 AA.

XX

AC ABM00062;

XX

DT 02-APR-2003 (first entry)

XX

DE Savinas antibody binding peptide sequence 16.

XX

KW Allergen; protein coordinate data; vaccine; antiallergic; immunogenicity;  
KW detergent; personal care composition; cosmetic.

XX

OS Unidentified.

XX

PN WO200183559-A2.

XX

PD 08-NOV-2001.

XX

PF 30-APR-2001; 2001WO-DK00293.

XX

PR 28-APR-2000; 2000DK-0000707.

PR 10-MAY-2000; 2000US-203345P.

PR 28-FEB-2001; 2001DK-0000327.

PR 21-MAR-2001; 2001US-277817P.

XX

PA (NOVO ) NOVOZYMES AS.

XX

PI Roggen EL, Ernst S, Svendsen A, Friis EP, Von Der Osten C;

XX

DR WPI; 2001-626552/72.

XX

PT Selecting protein variants having modified immunogenicity, used to  
PT produce vaccines, detergents and personal care compositions, involves  
PT localizing epitope sequences on the three-dimensional structure of a  
PT protein -

XX

PS Example 1; Page 143; 513pp; English.

XX

CC The invention relates to selecting a protein variant having modified  
CC immunogenicity, compared to a parent protein, comprising using the  
CC antibody binding sequence to localise epitope sequences on the three  
CC dimensional structure of the parent protein and defining an epitope area  
CC including amino acids within 5 Angstrom of the epitope amino acids. The  
CC method is useful for identifying structural epitopes on the 3-dimensional  
CC surface of commercial and environmental allergens. Compositions  
CC containing the protein variants are used as vaccines, detergents and  
CC personal care compositions, e.g. shampoo, balsam, hair conditioners, hair  
CC waving compositions, hair dyeing compositions, hair tonic, hair liquid,  
CC hair cream, hair rinse, hair spray, chewing gum, skin cream, sunscreen,  
CC shaving foam, cream soap, skin milk or foundation. The present sequence  
CC is that of an antibody binding peptide sequence related to the invention.

XX

SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4

|||

Db 2 VLR 4

#### RESULT 21

ABM00074

ID ABM00074 standard; Peptide; 6 AA.

XX

AC ABM00074;

XX

DT 02-APR-2003 (first entry)

XX

DE Savinas antibody binding peptide sequence 28.

XX

KW Allergen; protein coordinate data; vaccine; antiallergic; immunogenicity;

KW detergent; personal care composition; cosmetic.

XX

OS Unidentified.

XX

PN WO200183559-A2.

XX

PD 08-NOV-2001.

XX

PF 30-APR-2001; 2001WO-DK00293.

XX

PR 28-APR-2000; 2000DK-0000707.

PR 10-MAY-2000; 2000US-203345P.

PR 28-FEB-2001; 2001DK-0000327.

PR 21-MAR-2001; 2001US-277817P.

XX

PA (NOVO ) NOVOZYMES AS.

XX

PI Roggen EL, Ernst S, Svendsen A, Friis EP, Von Der Osten C;

XX

DR WPI; 2001-626552/72.  
 XX  
 PT Selecting protein variants having modified immunogenicity, used to  
 PT produce vaccines, detergents and personal care compositions, involves  
 PT localizing epitope sequences on the three-dimensional structure of a  
 PT protein -  
 XX  
 PS Example 1; Page 143; 513pp; English.  
 XX  
 CC The invention relates to selecting a protein variant having modified  
 CC immunogenicity, compared to a parent protein, comprising using the  
 CC antibody binding sequence to localise epitope sequences on the three  
 CC dimensional structure of the parent protein and defining an epitope area  
 CC including amino acids within 5 Angstrom of the epitope amino acids. The  
 CC method is useful for identifying structural epitopes on the 3-dimensional  
 CC surface of commercial and environmental allergens. Compositions  
 CC containing the protein variants are used as vaccines, detergents and  
 CC personal care compositions, e.g. shampoo, balsam, hair conditioners, hair  
 CC waving compositions, hair dyeing compositions, hair tonic, hair liquid,  
 CC hair cream, hair rinse, hair spray, chewing gum, skin cream, sunscreen,  
 CC shaving foam, cream soap, skin milk or foundation. The present sequence  
 CC is that of an antibody binding peptide sequence related to the invention.  
 XX  
 SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 2 VLR 4

# RESULT 22

AAU03882

ID AAU03882 standard; Peptide; 6 AA.

XX

AC AAU03882;

XX

DT 12-SEP-2001 (first entry)

XX

DE G protein-coupled receptor-like (GPCR-like) receptor binding peptide #52.

XX

KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
 KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
 KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;  
 KW fruitfly.

XX

OS Synthetic.

XX

PN WO200138533-A2.

XX

PD 31-MAY-2001.

XX

PF 24-NOV-2000; 2000WO-US32225.

XX



PR 24-NOV-1999; 99US-0167523.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN.  
 XX  
 PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;  
 XX  
 DR WPI; 2001-343952/36.  
 XX  
 PT Using G-protein-coupled receptor (GPCR)-like receptors to identify  
 PT candidate compounds for the treatment and prevention of invertebrate  
 PT parasites, especially helminths and insects -  
 XX  
 PS Claim 14; Page 56; 219pp; English.  
 XX  
 CC The sequence represents a G protein-coupled receptor-like (GPCR-like)  
 CC receptor protein. GPCR-like receptors and their associated nucleic acids  
 CC may be used to identify candidate compounds for their ability to modulate  
 CC the activity of GPCRs. The sequences therefore are useful for treating  
 CC and preventing infection by endoparasitic and ectoparasitic invertebrate  
 CC parasites, especially helminths and insects, and particularly ailments  
 CC related to aberrant neurological and neuromuscular function.  
 XX  
 SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 3 VLR 5

# RESULT 23

AAU03890

ID AAU03890 standard; Peptide; 6 AA.

XX

AC AAU03890;

XX

DT 12-SEP-2001 (first entry)

XX

DE G protein-coupled receptor-like (GPCR-like) receptor binding peptide #60.

XX

KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
 KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
 KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;  
 KW fruitfly.

XX

OS Synthetic.

XX

PN WO200138533-A2.

XX

PD 31-MAY-2001.

XX

PF 24-NOV-2000; 2000WO-US32225.

XX

PR 24-NOV-1999; 99US-0167523.

XX  
PA (PHAA ) PHARMACIA & UPJOHN.  
XX  
PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;  
XX  
DR WPI; 2001-343952/36.  
XX  
PT Using G-protein-coupled receptor (GPCR)-like receptors to identify  
PT candidate compounds for the treatment and prevention of invertebrate  
PT parasites, especially helminths and insects -  
XX  
PS Claim 14; Page 56; 219pp; English.  
XX  
CC The sequence represents a G protein-coupled receptor-like (GPCR-like)  
CC receptor protein. GPCR-like receptors and their associated nucleic acids  
CC may be used to identify candidate compounds for their ability to modulate  
CC the activity of GPCRs. The sequences therefore are useful for treating  
CC and preventing infection by endoparasitic and ectoparasitic invertebrate  
CC parasites, especially helminths and insects, and particularly ailments  
CC related to aberrant neurological and neuromuscular function.  
XX  
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

# RESULT 24

AAU03891

ID AAU03891 standard; Peptide; 6 AA.

XX

AC AAU03891;

XX

DT 12-SEP-2001 (first entry)

XX

DE G protein-coupled receptor-like (GPCR-like) receptor binding peptide #61.

XX

KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;  
KW fruitfly.

XX

OS Synthetic.

XX

PN WO200138533-A2.

XX

PD 31-MAY-2001.

XX

PF 24-NOV-2000; 2000WO-US32225.

XX

PR 24-NOV-1999; 99US-0167523.

XX

PA (PHAA ) PHARMACIA & UPJOHN.  
XX  
PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;  
XX  
DR WPI; 2001-343952/36.  
XX  
PT Using G-protein-coupled receptor (GPCR)-like receptors to identify  
PT candidate compounds for the treatment and prevention of invertebrate  
PT parasites, especially helminths and insects -  
XX  
PS Claim 14; Page 56; 219pp; English.  
XX  
CC The sequence represents a G protein-coupled receptor-like (GPCR-like)  
CC receptor protein. GPCR-like receptors and their associated nucleic acids  
CC may be used to identify candidate compounds for their ability to modulate  
CC the activity of GPCRs. The sequences therefore are useful for treating  
CC and preventing infection by endoparasitic and ectoparasitic invertebrate  
CC parasites, especially helminths and insects, and particularly ailments  
CC related to aberrant neurological and neuromuscular function.  
XX  
SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 25  
AAU97098

ID AAU97098 standard; Peptide; 6 AA.  
XX  
AC AAU97098;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE Absciscic acid (ABA) hydroxylase, conserved motif #1.  
XX  
KW ABA hydroxylase; absciscic acid hydroxylase; transgenic; plant;  
KW enzyme.  
XX  
OS Synthetic.  
XX  
PN WO200246377-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 06-DEC-2001; 2001WO-CA01756.  
XX  
PR 07-DEC-2000; 2000US-251518P.  
XX  
PA (CANA ) NAT RES COUNCIL CANADA.  
XX  
PI Krochko JE, Cutler AJ, Abrams SR;

XX  
 DR WPI; 2002-519663/55.  
 XX  
 PT New isolated and purified DNA that encodes protein having abscisic  
 PT acid (ABA) hydroxylase activity, useful for altering catabolism of  
 PT abscisic acid in plants -  
 XX  
 PS Claim 3; Page 72; 117pp; English.  
 XX  
 CC The invention relates to an isolated and purified DNA (I) that encodes a  
 CC protein having abscisic acid (ABA) hydroxylase activity. (I) is useful  
 CC for producing a transgenic plant which involves introducing (I) into a  
 CC genome of the plant or its part, and carrying out plant growth and  
 CC development. (I) is useful for modifying catabolism of ABA or ABA  
 CC analogues in a plant. ABA hydroxylase clone pBE10-30-3 cDNA sequence  
 CC is useful for identification of related sequences from other plant  
 CC species. (I) is also useful for altering ABA and ABA analog catabolism  
 CC in plants. The present sequence represents abscisic acid (ABA)  
 CC hydroxylase conserved motif #1.  
 XX  
 SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 2 VLR 4

# RESULT 26

AAM47693

ID AAM47693 standard; Peptide; 6 AA.

XX

AC AAM47693;

XX

DT 22-FEB-2002 (first entry)

XX

DE Human HARE peptide fragment PR 1869 #2.

XX

KW HARE; Hyaluronic Acid Receptor for Endocytosis; hyaluronan; chondroitin;  
 KW chondroitin sulphate; extracellular matrix; cartilage; skin; human; rat;  
 KW vitreous humour; endocytic receptor; glycosaminoglycan.

XX

OS Homo sapiens.

XX

PN WO200181544-A2.

XX

PD 01-NOV-2001.

XX

PF 25-APR-2001; 2001WO-US13403.

XX

PR 25-APR-2000; 2000US-199538P.

PR 02-NOV-2000; 2000US-245320P.

XX

PA (WEIG/) WEIGEL P A.

PA (ZHOU/) ZHOU B.  
 PA (WEIG/) WEIGEL J A.  
 XX  
 PI Weigel PA, Zhou B, Weigel JA;  
 XX  
 DR WPI; 2002-049271/06.  
 XX  
 PT New mammalian hyaluronic acid receptor for endocytosis, useful e.g. for  
 PT identifying agents that inhibit binding to hyaluronic acid, and related  
 PT nucleic acid -  
 XX  
 PS Example; Page 94; 263pp; English.  
 XX  
 CC The present invention relates to sequences for rat and human HARE  
 CC (Hyaluronic Acid Receptor for Endocytosis, ABA04648, ABA04662, AAM47675  
 CC and AAM47684). HARE can bind specifically to at least one of hyaluronic  
 CC acid (HA, also known as hyaluronan), chondroitin (C) or chondroitin  
 CC sulphate (CS). HA is an extracellular matrix component of all tissues,  
 CC in particular cartilage, skin and vitreous humour. HARE is the endocytic  
 CC receptor responsible for removing HA and other glycosaminoglycans from  
 CC the circulation. The present sequence is a peptide fragment of HARE,  
 CC which was used in an example from the present invention.  
 XX  
 SQ Sequence 6 AA;

Query Match 60.0%; Score 3; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 4 VLR 6

# RESULT 27

AAW51299

ID AAW51299 standard; peptide; 7 AA.

XX

AC AAW51299;

XX

DT 15-SEP-1998 (first entry)

XX

DE Human B-type natriuretic peptide variant, C-terminal sequence.

XX

KW B-type natriuretic peptide; clearance receptor; electrolyte balance;

KW diuretic; vasodilator; circulation; natriuresis; diuresis; hNPR-C;

KW cyclic guanosine monophosphate; cGMP; second messenger; variant.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /label= Asn, Lys

FT Misc-difference 5

FT /label= Arg, Lys

XX

PN WO9817690-A1.

XX  
PD 30-APR-1998.  
XX  
PF 09-OCT-1997; 97WO-US18384.  
XX  
PR 22-OCT-1996; 96US-0731880.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Lowe DG, Schoenfeld JR;  
XX  
DR WPI; 1998-261429/23.  
XX  
PT Variants of brain natriuretic peptide with reduced affinity for  
PT clearance receptor - for treating disorders of electrolyte balance  
PT and as diuretics and vasodilators, have increased circulation time  
PT and in vivo activity  
XX  
PS Disclosure; Page 8; 55pp; English.  
XX  
CC The invention relates to variants of brain natriuretic peptide (BNP)  
CC with reduced affinity for the human clearance receptor (hNPR-C) relative  
CC to wild-type BNP. The variants are used: (a) to treat or prevent  
CC disorders of electrolyte balance, or (b) to induce natriuresis, diuresis  
CC or vasodilation. Typical applications are in congestive heart failure,  
CC arrhythmia, hypertension, nephrotic syndrome, pre-eclampsia, premenstrual  
CC syndrome, hepatic cirrhosis, pulmonary disease and renal failure  
CC (associated with inefficient renal perfusion or reduced glomerular  
CC filtration rate). The variants are also useful as intermediates and as  
CC modulators of other compounds with similar activities. Although the  
CC variants have reduced affinity for NPR-C, they have at least equal  
CC affinity for the A receptor (NPR-A) and ability to stimulate cyclic  
CC guanosine monophosphate (cGMP), second messenger, production. The  
CC variants should persist for longer in the circulation and thus have  
CC greater in vivo activity. The present sequence represents the  
CC C-terminal sequence of a BNP variant.  
XX  
SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 19; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

# RESULT 28

AAY41942

ID AAY41942 standard; Peptide; 7 AA.

XX

AC AAY41942;

XX

DT 09-DEC-1999 (first entry)

XX

DE Rheumatoid arthritis diagnostic protein isoform peptide #93.

XX  
 KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;  
 KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;  
 KW rheumatoid arthritis diagnostic protein isoform; screening;  
 KW expression reference protein isoform; prognosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9947925-A2.  
 XX  
 PD 23-SEP-1999.  
 XX  
 PF 15-MAR-1999; 99WO-GB00763.  
 XX  
 PR 13-MAR-1998; 98GB-0005477.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Parekh RB, Patel TP, Townsend RR;  
 XX  
 DR WPI; 1999-571871/48.  
 XX  
 PT Diagnosis of human rheumatoid arthritis by two-dimensional  
 PT electrophoresis -  
 XX  
 PS Disclosure; Page 19; 157pp; English.  
 XX  
 CC A method has been developed for the diagnosis of human rheumatoid  
 CC arthritis (RA) using two-dimensional electrophoresis to generate a  
 CC two-dimensional array of features. The method can be used for screening,  
 CC diagnosis and prognosis of RA in a subject or for monitoring the effect  
 CC of an anti-RA drug or therapy administered to a subject. The method  
 CC comprises: (a) analysing a sample of serum or plasma and optionally  
 CC synovial fluid by two-dimensional electrophoresis, to generate a two-  
 CC dimensional array of features; (b) identifying at least one chosen  
 CC feature whose relative abundance correlates with the presence or absence  
 CC of RA; and (c) comparing the abundance of each chosen feature in the  
 CC sample with the abundance of that chosen feature in serum or plasma from  
 CC one or more persons without RA, where the relative abundance of the  
 CC chosen feature or features in the sample indicates the presence or  
 CC absence of RA in the subject. The method can also be used in clinical  
 CC studies for testing drugs for therapy of RA, for purification of RA-  
 CC diagnostic protein isoforms (RPIs), and for production of antibodies to  
 CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify  
 CC compounds that promote or inhibit their activity, which are then used as  
 CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy  
 CC protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to  
 CC AAY42103 represent expression reference protein isoform peptides and  
 CC AAZ25066 to AAZ25068 represent degenerate probes for RPIs, which are all  
 CC used in the exemplification of the present invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            2 VLR 4  
              |||  
Db            5 VLR 7

RESULT 29

AAy14768

ID    AAY14768 standard; peptide; 7 AA.

XX

AC    AAY14768;

XX

DT    11-OCT-1999    (first entry)

XX

DE    P450 enzyme conserved peptide motif.

XX

KW    Genetic proximity; gene expression; cell characterisation; homeobox gene;

KW    genetic defect; reverse transcriptase polymerase chain reaction; RT-PCR;

KW    kinase gene; protein phosphatase; P450; steroid receptor; cadherin.

XX

OS    Homo sapiens.

XX

PN    WO9934016-A2.

XX

PD    08-JUL-1999.

XX

PF    28-DEC-1998;    98WO-IL00625.

XX

PR    16-OCT-1998;    98IL-0126627.

PR    29-DEC-1997;    97IL-0122793.

XX

PA    (GENE-) GENENA LTD.

XX

PI    Vider B;

XX

DR    WPI; 1999-419113/35.

DR    N-PSDB; AAZ18246.

XX

PT    Identifying and characterizing cells by comparing the pattern of

PT    gene expression in a selected gene family

XX

PS    Examples; Page 50; 102pp; English.

XX

CC    The invention provides a new method for identifying and characterising  
CC    cells. The method for determining the genetic proximity of a first cell  
CC    and a second cell comprises: (a) obtaining the first cell and the second  
CC    cell; (b) determining in the first cell and the second cell the pattern  
CC    of expression of genes in a selected gene family; and (c) calculating a  
CC    proximity index using a specified formula. The methods can be used for  
CC    characterising cells, e.g. for determining the origin of a cell, its  
CC    genetic status, whether it carries a genetic defect, or whether it is  
CC    transformed. They can be used for detecting a selected genetic defect in  
CC    an individual, e.g. a fetus. They can also be used for determining the  
CC    effect of a selected treatment on a test cell. They can also be used for  
CC    obtaining cells capable of expressing an homeobox related desired  
CC    property. The method uses reverse transcriptase polymerase chain  
CC    reaction (RT-PCR) for determining the pattern of gene expression in a  
CC    selected gene family. Sequences AAZ17803-Z18342 represent primers that



CC can be used in the RT-PCR reactions to determine the pattern of gene  
CC expression. The gene family can be selected from a set of homeobox genes,  
CC kinase genes, protein phosphatase genes, P450 enzyme genes, steroid  
CC receptor superfamily genes or cadherin superfamily genes. Sequences  
CC AAY14603-813 represent conserved peptide motifs based on which the  
CC primers of the invention were designed.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 20; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4

|||

Db 5 VLR 7

# RESULT 30

AAY16932

ID AAY16932 standard; peptide; 7 AA.

XX

AC AAY16932;

XX

DT 20-JUL-1999 (first entry)

XX

DE Heat shock protein (hsp) binding peptide.

XX

KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;  
KW surface protein; tethering peptide; chaperone process; cytokine; cancer;  
KW neoplastic disease; infectious disease; bacterium; immune system; fungus;  
KW acquired immune deficiency; autoimmune disease.

XX

OS Synthetic.

XX

PN WO9922761-A1.

XX

PD 14-MAY-1999.

XX

PF 22-OCT-1998; 98WO-US22335.

XX

PR 31-OCT-1997; 97US-0961707.

XX

PA (SLOK ) SLOAN KETTERING INST CANCER RES.

XX

PI Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;

PI Ouerfelli O, Rothman JE;

XX

DR WPI; 1999-313177/26.

XX

PT Identifying peptides which bind heat shock proteins

XX

PS Examples; Page 21; 155pp; English.

XX

CC The invention relates to conjugate peptides engineered to noncovalently  
CC bind to heat shock proteins (hsp). A method of identifying a hsp binding  
CC peptide comprises (a) contacting a phage display library having

CC bacteriophage expressing, in a surface protein, inserted peptides with a  
 CC hsp target, and bound to a benzoquinone ansamycin antibiotic (BAA), in a  
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp  
 CC target; and (c) identifying the inserted peptide expressed. The peptides  
 CC which bind to a hsp can be used as tethering peptides for a hsp which may  
 CC serve as an accessory in a chaperone process and/or may comprise a  
 CC cytokine. They can also be coupled to antigens to induce an immune  
 CC response. Such compositions can be used for treating neoplastic disease,  
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,  
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a  
 CC disease of the immune system, e.g. acquired immune deficiencies or  
 CC autoimmune diseases.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 4 VLR 6

# RESULT 31

AAY16976

ID AAY16976 standard; peptide; 7 AA.

XX

AC AAY16976;

XX

DT 20-JUL-1999 (first entry)

XX

DE Heat shock protein (hsp) binding peptide.

XX

KW Conjugate peptide; heat shock protein; hsp; phage display library; virus;  
 KW surface protein; tethering peptide; chaperone process; cytokine; cancer;  
 KW neoplastic disease; infectious disease; bacterium; immune system; fungus;  
 KW acquired immune deficiency; autoimmune disease.

XX

OS Synthetic.

XX

PN WO9922761-A1.

XX

PD 14-MAY-1999.

XX

PF 22-OCT-1998; 98WO-US22335.

XX

PR 31-OCT-1997; 97US-0961707.

XX

PA (SLOK ) SLOAN KETTERING INST CANCER RES.

XX

PI Hartl U, Hoe MH, Houghton A, Mayhew M, Moroi Y;

PI Ouerfelli O, Rothman JE;

XX

DR WPI; 1999-313177/26.

XX

PT Identifying peptides which bind heat shock proteins

XX  
 PS Examples; Page 23; 155pp; English.  
 XX  
 CC The invention relates to conjugate peptides engineered to noncovalently  
 CC bind to heat shock proteins (hsp). A method of identifying a hsp binding  
 CC peptide comprises (a) contacting a phage display library having  
 CC bacteriophage expressing, in a surface protein, inserted peptides with a  
 CC hsp target, and bound to a benzoquinone ansamycin antibiotic (BAA), in a  
 CC physiologic binding buffer; (b) isolating a phage binding to the hsp  
 CC target; and (c) identifying the inserted peptide expressed. The peptides  
 CC which bind to a hsp can be used as tethering peptides for a hsp which may  
 CC serve as an accessory in a chaperone process and/or may comprise a  
 CC cytokine. They can also be coupled to antigens to induce an immune  
 CC response. Such compositions can be used for treating neoplastic disease,  
 CC e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium,  
 CC virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a  
 CC disease of the immune system, e.g. acquired immune deficiencies or  
 CC autoimmune diseases.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 5 VLR 7

RESULT 32

AAY80233

ID AAY80233 standard; peptide; 7 AA.

XX

AC AAY80233;

XX

DT 25-MAY-2000 (first entry)

XX

DE B-type natriuretic peptide variant C-terminal peptide SEQ ID NO:42.

XX

KW Human; B-type natriuretic peptide; BNP; clearance receptor; diuretic;  
 KW water imbalance; electrolyte imbalance; natriuretic peptide receptor;  
 KW natriuresis; diuresis; vasodilation; hypotensive; cardiant; hepatotropic;  
 KW nephrotropic; vasorelaxant; hypertension; congestive heart failure;  
 KW nephrotic syndrome; hepatic cirrhosis; pulmonary disease; renal failure.

XX

OS Mammalia.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /label= Asn, Lys

FT Misc-difference 5

FT /label= Arg, Lys

XX

PN US6028055-A.

XX

PD 22-FEB-2000.

XX  
 PF 21-OCT-1997; 97US-0954915.  
 XX  
 PR 22-OCT-1996; 96US-0028854.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Schoenfeld JR, Lowe DG;  
 XX  
 DR WPI; 2000-194846/17.  
 XX  
 PT B-type natriuretic peptide (BNP) variant (I) having a decreased binding  
 PT affinity for the human clearance receptor, useful for treating  
 PT natriuresis, diuresis or vasodilation -  
 XX  
 PS Disclosure; Column 8; 33pp; English.  
 XX  
 CC The present invention describes a B-type natriuretic peptide (BNP)  
 CC variant (I) having a decreased binding affinity for the human clearance  
 CC receptor compared to human wild-type BNP. The present invention also  
 CC describes a method for treating a disorder of electrolyte balance  
 CC including natriuresis, diuresis or vasodilation comprising administering  
 CC a composition comprising (I). (I) has hypotensive, cardiant,  
 CC hepatotropic, nephrotropic, natriuretic, diuretic and vasorelaxant  
 CC activities. (I) can be used for the treatment or prophylaxis of  
 CC conditions associated with water or electrolyte imbalance and  
 CC hypertension, such as congestive heart failure (CHF), nephrotic syndrome  
 CC and hepatic cirrhosis, pulmonary disease, and renal failure due to  
 CC ineffective renal perfusion or reduced glomerular filtration rate. (I)  
 CC can also useful for treating natriuresis, diuresis or vasodilation.  
 CC The present sequence represents an C-terminal peptide from a BNP  
 CC variant given in the present invention.  
 XX  
 SQ Sequence 7 AA;  
  
 Query Match 60.0%; Score 3; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 VLR 4  
 |||  
 Db 2 VLR 4

# RESULT 33

AAU72074  
 ID AAU72074 standard; Peptide; 7 AA.  
 XX  
 AC AAU72074;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE Melanoma antigen, javelin peptide #60.  
 XX  
 KW Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;  
 KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYEs01; GM2;  
 KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;

KW javelin molecule; melanoma antigen recognised by T cells-1; human.  
 XX  
 OS Bacteriophage M13.  
 XX  
 PN WO200178655-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 17-APR-2001; 2001WO-US12449.  
 XX  
 PR 17-APR-2000; 2000US-197462P.  
 XX  
 PA (HOUG/) HOUGHTON A.  
 PA (LIVI/) LIVINGSTON P.  
 PA (ALAW/) AL-AWQATI Q.  
 PA (MAYH/) MAYHEW M.  
 PA (HOEM/) HOE M.  
 XX  
 PI Houghton A, Livingston P, Al-awqati Q, Mayhew M, Hoe M;  
 XX  
 DR WPI; 2001-663092/76.  
 XX  
 PT Anti cancer vaccine for the treatment of melanoma comprises a heat  
 PT shock protein and a melanoma antigen i.e. tyrosinase -  
 XX  
 PS Disclosure; Page 17; 150pp; English.  
 XX  
 CC The invention relates to a method of induction of an immune response,  
 CC comprising administration of an immunotherapeutic composition, comprising  
 CC a heat shock protein, and a melanoma antigen, where the melanoma  
 CC antigen is selected from tyrosinase, tyrosinase related protein 1,  
 CC tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens,  
 CC NYEs01, MART antigens, GM2, antigenic portions and combinations of these.  
 CC The melanoma antigen is covalently bound to a javelin molecule, where the  
 CC melanoma antigen bound to the javelin molecule is non-covalently bound to  
 CC the heat shock protein. The composition is useful for inducing an immune  
 CC response for the treatment of melanoma. AAU71980-AAU72481 represent  
 CC melanoma antigen peptides of the invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
 |||  
 Db 4 VLR 6

RESULT 34  
 AAU72118  
 ID AAU72118 standard; Peptide; 7 AA.  
 XX  
 AC AAU72118;  
 XX  
 DT 26-FEB-2002 (first entry)

XX  
 DE Melanoma antigen, javelin peptide #104.  
 XX  
 KW Melanoma antigen; MART-1; MAGE-1; gp100; cytostatic; immune response;  
 KW immunotherapeutic; heat shock protein; tyrosinase; BAGE; NYEs01; GM2;  
 KW tyrosinase related protein 1; tyrosinase related protein 2; vaccine;  
 KW javelin molecule; melanoma antigen recognised by T cells-1; human.  
 XX  
 OS Bacteriophage M13.  
 XX  
 PN WO200178655-A2.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 17-APR-2001; 2001WO-US12449.  
 XX  
 PR 17-APR-2000; 2000US-197462P.  
 XX  
 PA (HOUG/) HOUGHTON A.  
 PA (LIVI/) LIVINGSTON P.  
 PA (ALAW/) AL-AWQATI Q.  
 PA (MAYH/) MAYHEW M.  
 PA (HOEM/) HOE M.  
 XX  
 PI Houghton A, Livingston P, Al-awqati Q, Mayhew M, Hoe M;  
 XX  
 DR WPI; 2001-663092/76.  
 XX  
 PT Anti cancer vaccine for the treatment of melanoma comprises a heat  
 PT shock protein and a melanoma antigen i.e. tyrosinase -  
 XX  
 PS Disclosure; Page 18; 150pp; English.  
 XX  
 CC The invention relates to a method of induction of an immune response,  
 CC comprising administration of an immunotherapeutic composition, comprising  
 CC a heat shock protein, and a melanoma antigen, where the melanoma  
 CC antigen is selected from tyrosinase, tyrosinase related protein 1,  
 CC tyrosinase related protein 2, gp 100, MAGE antigens, BAGE antigens,  
 CC NYEs01, MART antigens, GM2, antigenic portions and combinations of these.  
 CC The melanoma antigen is covalently bound to a javelin molecule, where the  
 CC melanoma antigen bound to the javelin molecule is non-covalently bound to  
 CC the heat shock protein. The composition is useful for inducing an immune  
 CC response for the treatment of melanoma. AAU71980-AAU72481 represent  
 CC melanoma antigen peptides of the invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 5 VLR 7

AAU03883  
 ID AAU03883 standard; Peptide; 7 AA.  
 XX  
 AC AAU03883;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE G protein-coupled receptor-like (GPCR-like) receptor binding peptide #53.  
 XX  
 KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
 KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
 KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;  
 KW fruitfly.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200138533-A2.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PF 24-NOV-2000; 2000WO-US32225.  
 XX  
 PR 24-NOV-1999; 99US-0167523.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN.  
 XX  
 PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;  
 XX  
 DR WPI; 2001-343952/36.  
 XX  
 PT Using G-protein-coupled receptor (GPCR)-like receptors to identify  
 PT candidate compounds for the treatment and prevention of invertebrate  
 PT parasites, especially helminths and insects -  
 XX  
 PS Claim 14; Page 56; 219pp; English.  
 XX  
 CC The sequence represents a G protein-coupled receptor-like (GPCR-like)  
 CC receptor protein. GPCR-like receptors and their associated nucleic acids  
 CC may be used to identify candidate compounds for their ability to modulate  
 CC the activity of GPCRs. The sequences therefore are useful for treating  
 CC and preventing infection by endoparasitic and ectoparasitic invertebrate  
 CC parasites, especially helminths and insects, and particularly ailments  
 CC related to aberrant neurological and neuromuscular function.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
 |||  
 Db 4 VLR 6

RESULT 36  
 AAU03884

ID AAU03884 standard; Peptide; 7 AA.  
 XX  
 AC AAU03884;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE G protein-coupled receptor-like (GPCR-like) receptor binding peptide #54.  
 XX  
 KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
 KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
 KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;  
 KW fruitfly.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200138533-A2.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PF 24-NOV-2000; 2000WO-US32225.  
 XX  
 PR 24-NOV-1999; 99US-0167523.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN.  
 XX  
 PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;  
 XX  
 DR WPI; 2001-343952/36.  
 XX  
 PT Using G-protein-coupled receptor (GPCR)-like receptors to identify  
 PT candidate compounds for the treatment and prevention of invertebrate  
 PT parasites, especially helminths and insects -  
 XX  
 PS Claim 14; Page 56; 219pp; English.  
 XX  
 CC The sequence represents a G protein-coupled receptor-like (GPCR-like)  
 CC receptor protein. GPCR-like receptors and their associated nucleic acids  
 CC may be used to identify candidate compounds for their ability to modulate  
 CC the activity of GPCRs. The sequences therefore are useful for treating  
 CC and preventing infection by endoparasitic and ectoparasitic invertebrate  
 CC parasites, especially helminths and insects, and particularly ailments  
 CC related to aberrant neurological and neuromuscular function.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
 |||  
 Db 4 VLR 6

RESULT 37

AAU03888

ID AAU03888 standard; Peptide; 7 AA.



XX  
 AC AAU03888;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE G protein-coupled receptor-like (GPCR-like) receptor binding peptide #58.  
 XX  
 KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
 KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
 KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;  
 KW fruitfly.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200138533-A2.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PF 24-NOV-2000; 2000WO-US32225.  
 XX  
 PR 24-NOV-1999; 99US-0167523.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN.  
 XX  
 PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;  
 XX  
 DR WPI; 2001-343952/36.  
 XX  
 PT Using G-protein-coupled receptor (GPCR)-like receptors to identify  
 PT candidate compounds for the treatment and prevention of invertebrate  
 PT parasites, especially helminths and insects -  
 XX  
 PS Claim 14; Page 56; 219pp; English.  
 XX  
 CC The sequence represents a G protein-coupled receptor-like (GPCR-like)  
 CC receptor protein. GPCR-like receptors and their associated nucleic acids  
 CC may be used to identify candidate compounds for their ability to modulate  
 CC the activity of GPCRs. The sequences therefore are useful for treating  
 CC and preventing infection by endoparasitic and ectoparasitic invertebrate  
 CC parasites, especially helminths and insects, and particularly ailments  
 CC related to aberrant neurological and neuromuscular function.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
 |||  
 Db 4 VLR 6

RESULT 38  
 AAU03889  
 ID AAU03889 standard; Peptide; 7 AA.  
 XX

AC AAU03889;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE G protein-coupled receptor-like (GPCR-like) receptor binding peptide #59.  
 XX  
 KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;  
 KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;  
 KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;  
 KW fruitfly.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200138533-A2.  
 XX  
 PD 31-MAY-2001.  
 XX  
 PF 24-NOV-2000; 2000WO-US32225.  
 XX  
 PR 24-NOV-1999; 99US-0167523.  
 XX  
 PA (PHAA ) PHARMACIA & UPJOHN.  
 XX  
 PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;  
 XX  
 DR WPI; 2001-343952/36.  
 XX  
 PT Using G-protein-coupled receptor (GPCR)-like receptors to identify  
 PT candidate compounds for the treatment and prevention of invertebrate  
 PT parasites, especially helminths and insects -  
 XX  
 PS Claim 14; Page 56; 219pp; English.  
 XX  
 CC The sequence represents a G protein-coupled receptor-like (GPCR-like)  
 CC receptor protein. GPCR-like receptors and their associated nucleic acids  
 CC may be used to identify candidate compounds for their ability to modulate  
 CC the activity of GPCRs. The sequences therefore are useful for treating  
 CC and preventing infection by endoparasitic and ectoparasitic invertebrate  
 CC parasites, especially helminths and insects, and particularly ailments  
 CC related to aberrant neurological and neuromuscular function.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
 |||  
 Db 4 VLR 6

RESULT 39  
 AAB98053  
 ID AAB98053 standard; peptide; 7 AA.  
 XX  
 AC AAB98053;

XX  
 DT 15-AUG-2001 (first entry)  
 XX  
 DE Rat endoproteinase peptide SEQ ID NO:6.  
 XX  
 KW Galactosaminoglycan 4-sulphate group transferase; G4ST; sulphate donor;  
 KW N-acetylgalactosamine; galactosaminoglycan.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN JP2001061481-A.  
 XX  
 PD 13-MAR-2001.  
 XX  
 PF 27-AUG-1999; 99JP-0241312.  
 XX  
 PR 27-AUG-1999; 99JP-0241312.  
 XX  
 PA (SE GK ) SEIKAGAKU KOGYO CO LTD.  
 XX  
 DR WPI; 2001-294710/31.  
 XX  
 PT A DNA encoding sulfate group transferase cDNA can be used for a large  
 PT scale preparation of galactosaminoglycan 4-sulfate group transferase  
 PT (G4ST) -  
 XX  
 PS Example 1; Page 11; 23pp; Japanese.  
 XX  
 CC The present invention describes a galactosaminoglycan 4-sulphate group  
 CC transferase (G4ST) protein with an activity of transferring a sulphate  
 CC group from a sulphate group donor to the 4-OH of N-acetylgalactosamine  
 CC residue contained in galactosaminoglycan. Polynucleotides encoding G4ST  
 CC can be used for large scale preparation of G4ST. The present sequence  
 CC represents an endoproteinase peptide which is used in an example from  
 CC the present invention.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 5 VLR 7

#### RESULT 40

AAB88610

ID AAB88610 standard; Peptide; 7 AA.

XX

AC AAB88610;

XX

DT 23-MAY-2001 (first entry)

XX

DE Human interleukin-6 receptor binding inhibitor #4.

XX

KW Interleukin-6; ligand; IL-6 receptor; antagonist; cancer; allergy;  
 KW rheumatoid arthritis; diabetes; multiple sclerosis; infection;  
 KW autoimmune disease; inflammatory disease.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200116166-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 25-AUG-2000; 2000WO-US23490.  
 XX  
 PR 27-AUG-1999; 99US-0151277.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Saxinger C;  
 XX  
 DR WPI; 2001-244395/25.  
 XX  
 PT Polypeptides which inhibit the binding of interleukin (IL)-6 ligand  
 PT with the IL-6 receptor, and the nucleic acids that encode them, useful  
 PT for treating e.g. inflammation and autoimmune diseases -  
 XX  
 PS Claim 37; Page 6; 98pp; English.  
 XX  
 CC The present invention describes a number of peptides which are able to  
 CC bind to the human interleukin-6 (IL-6) receptor and inhibit IL-6 binding.  
 CC These are useful in the treatment of diseases associated with abnormal  
 CC IL-6 expression, including multiple myeloma, plasmacytoma, haematological  
 CC diseases such as plasma cell dyscrasias, leukaemia and lymphoma,  
 CC mesangial proliferative glomerulonephritis, polyclonal B cell activation  
 CC conditions, allergies, rheumatoid arthritis, diabetes, multiple  
 CC sclerosis, septic shock, infections, post-menopausal osteoporosis,  
 CC chronic immune deficiency, autoimmune diseases and inflammatory diseases.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 4 VLR 6

RESULT 41  
 AAB88800  
 ID AAB88800 standard; Peptide; 7 AA.  
 XX  
 AC AAB88800;  
 XX  
 DT 23-MAY-2001 (first entry)  
 XX  
 DE Human interleukin-6 domain IV fragment #41.  
 XX

KW Interleukin-6; ligand; IL-6 receptor; antagonist; cancer; allergy;  
 KW rheumatoid arthritis; diabetes; multiple sclerosis; infection;  
 KW autoimmune disease; inflammatory disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200116166-A2.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 25-AUG-2000; 2000WO-US23490.  
 XX  
 PR 27-AUG-1999; 99US-0151277.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Saxinger C;  
 XX  
 DR WPI; 2001-244395/25.  
 XX  
 PT Polypeptides which inhibit the binding of interleukin (IL)-6 ligand  
 PT with the IL-6 receptor, and the nucleic acids that encode them, useful  
 PT for treating e.g. inflammation and autoimmune diseases -  
 XX  
 PS Example 4; Page 49; 98pp; English.  
 XX  
 CC The present invention describes a number of peptides which are able to  
 CC bind to the human interleukin-6 (IL-6) receptor and inhibit IL-6 binding.  
 CC These are useful in the treatment of diseases associated with abnormal  
 CC IL-6 expression, including multiple myeloma, plasmacytoma, haematological  
 CC diseases such as plasma cell dyscrasias, leukaemia and lymphoma,  
 CC mesangial proliferative glomerulonephritis, polyclonal B cell activation  
 CC conditions, allergies, rheumatoid arthritis, diabetes, multiple  
 CC sclerosis, septic shock, infections, post-menopausal osteoporosis,  
 CC chronic immune deficiency, autoimmune diseases and inflammatory diseases.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 1 VLR 3

#### RESULT 42

AAB49848

ID AAB49848 standard; Peptide; 7 AA.

XX

AC AAB49848;

XX

DT 02-MAR-2001 (first entry)

XX

DE Human endostatin peptide fragment SEQ ID NO: 61.

XX

KW Endostatin; antiangiogenic; angiogenesis; human; mouse; chicken;  
 KW cancer; inflammation; angiogenesis-dependent disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200067771-A1.  
 XX  
 PD 16-NOV-2000.  
 XX  
 PF 02-MAY-2000; 2000WO-US12063.  
 XX  
 PR 06-MAY-1999; 99US-0132907.  
 PR 14-JUL-1999; 99US-0353333.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Vuori K;  
 XX  
 DR WPI; 2001-040937/05.  
 XX  
 PT Endostatin peptide comprising at least four endostatin amino acid  
 PT residues are e.g. angiogenesis inhibitors for treating cancer and  
 PT diabetic retinopathy -  
 XX  
 PS Disclosure; Page 134; 146pp; English.  
 XX  
 CC The present invention provides endostatin peptides which can be used in  
 CC the modulation of angiogenesis. This is useful in the treatment of  
 CC cancers, inflammation, rheumatoid arthritis, chronic articular  
 CC rheumatism, psoriasis, disorders associated with inopportune invasion of  
 CC vessels such as diabetic retinopathy, neovascular glaucoma, retinopathy  
 CC of prematurity, macular degeneration, corneal graft rejection,  
 CC retrolental fibroplasia, rubeosis, capillary proliferation in  
 CC atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent  
 CC diseases include Osler-Webber syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophiliac joints and wound  
 CC granulation. In addition, the peptides can be used as birth control  
 CC agents.  
 XX  
 SQ Sequence 7 AA;  
  
 Query Match 60.0%; Score 3; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 VLR 4  
 |||  
 Db 5 VLR 7  
  
 RESULT 43  
 ABG77658  
 ID ABG77658 standard; Peptide; 7 AA.  
 XX  
 AC ABG77658;  
 XX  
 DT 05-NOV-2002 (first entry)

XX  
 DE Targetting peptide selective for human organ, tissue or cell type #191.  
 XX  
 KW Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;  
 KW immunomodulator; antibacterial; antiviral; gene therapy; cancer;  
 KW arthritis; diabetes; inflammatory disease; atherosclerosis;  
 KW autoimmune disease; bacterial infection; viral infection;  
 KW cardiovascular disease; degenerative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200220723-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 07-SEP-2001; 2001WO-US28044.  
 XX  
 PR 08-SEP-2000; 2000US-231266P.  
 PR 17-JAN-2001; 2001US-0765101.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Arap W, Pasqualini R;  
 XX  
 DR WPI; 2002-599247/64.  
 XX  
 PT New targeting peptides identified by phage display, useful for treating  
 PT a disease state, e.g. cancer, diabetes, inflammatory disease,  
 PT atherosclerosis, autoimmune disease, bacterial or viral infection or  
 PT cardiovascular disease -  
 XX  
 PS Claim 16; Fig 2B; 269pp; English.  
 XX  
 CC The invention describes an isolated peptide of 100 amino acids or less  
 CC in size. The peptide is useful for treating a disease state, e.g. cancer,  
 CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune  
 CC disease, bacterial infection, viral infection, cardiovascular disease  
 CC or degenerative disease. This sequence represents a human targeting  
 CC peptide selective for human organs, tissues or cell types.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
 |||  
 Db 5 VLR 7

# RESULT 44

ABG77669

ID ABG77669 standard; Peptide; 7 AA.

XX

AC ABG77669;

XX

DT 05-NOV-2002 (first entry)  
 XX  
 DE Targetting peptide selective for human organ, tissue or cell type #202.  
 XX  
 KW Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;  
 KW immunomodulator; antibacterial; antiviral; gene therapy; cancer;  
 KW arthritis; diabetes; inflammatory disease; atherosclerosis;  
 KW autoimmune disease; bacterial infection; viral infection;  
 KW cardiovascular disease; degenerative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200220723-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 07-SEP-2001; 2001WO-US28044.  
 XX  
 PR 08-SEP-2000; 2000US-231266P.  
 PR 17-JAN-2001; 2001US-0765101.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Arap W, Pasqualini R;  
 XX  
 DR WPI; 2002-599247/64.  
 XX  
 PT New targeting peptides identified by phage display, useful for treating  
 PT a disease state, e.g. cancer, diabetes, inflammatory disease,  
 PT atherosclerosis, autoimmune disease, bacterial or viral infection or  
 PT cardiovascular disease -  
 XX  
 PS Claim 16; Fig 2B; 269pp; English.  
 XX  
 CC The invention describes an isolated peptide of 100 amino acids or less  
 CC in size. The peptide is useful for treating a disease state, e.g. cancer,  
 CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune  
 CC disease, bacterial infection, viral infection, cardiovascular disease  
 CC or degenerative disease. This sequence represents a human targeting  
 CC peptide selective for human organs, tissues or cell types.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 2 VLR 4

RESULT 45

ABG77670

ID ABG77670 standard; Peptide; 7 AA.

XX

AC ABG77670;



XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Targetting peptide selective for human organ, tissue or cell type #203.  
 XX  
 KW Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;  
 KW immunomodulator; antibacterial; antiviral; gene therapy; cancer;  
 KW arthritis; diabetes; inflammatory disease; atherosclerosis;  
 KW autoimmune disease; bacterial infection; viral infection;  
 KW cardiovascular disease; degenerative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200220723-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 07-SEP-2001; 2001WO-US28044.  
 XX  
 PR 08-SEP-2000; 2000US-231266P.  
 PR 17-JAN-2001; 2001US-0765101.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Arap W, Pasqualini R;  
 XX  
 DR WPI; 2002-599247/64.  
 XX  
 PT New targeting peptides identified by phage display, useful for treating  
 PT a disease state, e.g. cancer, diabetes, inflammatory disease,  
 PT atherosclerosis, autoimmune disease, bacterial or viral infection or  
 PT cardiovascular disease -  
 XX  
 PS Claim 16; Fig 2B; 269pp; English.  
 XX  
 CC The invention describes an isolated peptide of 100 amino acids or less  
 CC in size. The peptide is useful for treating a disease state, e.g. cancer,  
 CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune  
 CC disease, bacterial infection, viral infection, cardiovascular disease  
 CC or degenerative disease. This sequence represents a human targeting  
 CC peptide selective for human organs, tissues or cell types.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
 |||  
 Db 4 VLR 6

RESULT 46  
 ABG77675  
 ID ABG77675 standard; Peptide; 7 AA.  
 XX

AC ABG77675;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Targetting peptide selective for human organ, tissue or cell type #208.  
 XX  
 KW Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;  
 KW immunomodulator; antibacterial; antiviral; gene therapy; cancer;  
 KW arthritis; diabetes; inflammatory disease; atherosclerosis;  
 KW autoimmune disease; bacterial infection; viral infection;  
 KW cardiovascular disease; degenerative disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200220723-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 07-SEP-2001; 2001WO-US28044.  
 XX  
 PR 08-SEP-2000; 2000US-231266P.  
 PR 17-JAN-2001; 2001US-0765101.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Arap W, Pasqualini R;  
 XX  
 DR WPI; 2002-599247/64.  
 XX  
 PT New targeting peptides identified by phage display, useful for treating  
 PT a disease state, e.g. cancer, diabetes, inflammatory disease,  
 PT atherosclerosis, autoimmune disease, bacterial or viral infection or  
 PT cardiovascular disease -  
 XX  
 PS Claim 16; Fig 2B; 269pp; English.  
 XX  
 CC The invention describes an isolated peptide of 100 amino acids or less  
 CC in size. The peptide is useful for treating a disease state, e.g. cancer,  
 CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune  
 CC disease, bacterial infection, viral infection, cardiovascular disease  
 CC or degenerative disease. This sequence represents a human targeting  
 CC peptide selective for human organs, tissues or cell types.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 4 VLR 6

RESULT 47  
 AAO17318  
 ID AAO17318 standard; Peptide; 7 AA.

XX  
 AC AAO17318;  
 XX  
 DT 08-JUL-2002 (first entry)  
 XX  
 DE A thaliana receptor kinase RKS13 peptide fragment.  
 XX  
 KW Vegetative propagation; plant; phytochrome; receptor kinase-like SERK;  
 KW RKS.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EP1094113-A1.  
 XX  
 PD 25-APR-2001.  
 XX  
 PF 22-OCT-1999; 99EP-0203480.  
 XX  
 PR 22-OCT-1999; 99EP-0203480.  
 XX  
 PA (GENE-) GENETWISTER TECHNOLOGIES BV.  
 XX  
 PI Schmidt EDL, Van Der Kop DAM, De Boer AD;  
 XX  
 DR WPI; 2002-228902/29.  
 XX  
 PT In vitro culture propagation of a plant from plant starting material,  
 PT comprises stimulating root/shoot initiation by introducing a  
 PT recombinant gene product into the starting material, thus reducing  
 PT phytochrome addition to culture -  
 XX  
 PS Disclosure; Page 112; 171pp; English.  
 XX  
 CC The present invention relates to a culture method for propagating a plant  
 CC from a plant starting material, where root or shoot initiation is  
 CC stimulated by introducing a gene into the starting material which allows  
 CC the reduction or absence of phytochrome addition to the culture. The  
 CC method is used for the propagation (preferably, seedless propagation) of  
 CC a plant from a plant starting material in an in vitro culture method.  
 CC Nucleic acids encoding receptor-like kinases are useful in the method.  
 CC The present sequence is a fragment of a receptor-like kinase protein.  
 XX  
 SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 4 VLR 6

RESULT 48  
 AAU79912  
 ID AAU79912 standard; Peptide; 7 AA.  
 XX

AC AAU79912;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Cassette mutagenesis wild-type pATP003.xb restriction site peptide #3.  
 XX  
 KW 2,5-diketo-D-gluconic acid reductase A enzyme; cofactor specificity site;  
 KW cofactor dependency; metabolically engineered organism; enzyme;  
 KW 2-keto-L-gluconic acid; glucose; single fermentation step;  
 KW cassette mutagenesis; restriction site; pATP003.xb.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200222527-A2.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 11-SEP-2001; 2001WO-US28366.  
 XX  
 PR 11-SEP-2000; 2000US-0658645.  
 XX  
 PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
 XX  
 PI Anderson S, Banta S;  
 XX  
 DR WPI; 2002-351864/38.  
 DR N-PSDB; ABK49072, ABK49073.  
 XX  
 PT Making mutant 2,5-diketo-D-gluconic acid reductase enzymes with altered  
 PT cofactor dependency, for producing 2-keto-L-gluconic acid from glucose  
 PT in one fermentation step, comprises mutating a cofactor specificity  
 PT site amino acid -  
 XX  
 PS Example 1; Page 34; 45pp; English.  
 XX  
 CC The present invention relates to a new method of producing mutant  
 CC 2,5-diketo-D-gluconic acid reductase enzymes with altered cofactor  
 CC dependency. The method of the invention involves identifying a cofactor  
 CC specificity site in a wild type 2,5-diketo-D-gluconic acid reductase  
 CC enzyme and mutating an amino acid in the identified cofactor specificity  
 CC site so that cofactor dependency of reactions catalysed by the enzyme is  
 CC altered. The method is useful for producing mutant 2,5-diketo-D-gluconic  
 CC acid reductase enzymes with altered cofactor dependency and as such is  
 CC useful in metabolically engineered organisms to produce 2-keto-L-gluconic  
 CC acid from glucose in a single fermentation step. The mutant 2,5-diketo-D-  
 CC gluconic acid reductase enzyme produces 2-keto-L-gluconic acid from  
 CC glucose in a single fermentation step in metabolically engineered  
 CC organisms. Flexibility in catalysing the enzymatic reaction by the enzyme  
 CC with NADH or nonspecifically with NADH (reduced nicotinamide adenine  
 CC dinucleotide) or NADPH provides advantages. Since the cost of NADPH is an  
 CC order of magnitude greater than that of NADH, use of the enzyme of the  
 CC invention in any in vitro system where cofactor must be purchased and  
 CC provided for the enzymes provides a significant cost saving advantage.  
 CC The mutant 2,5-diketo-D-gluconic acid reductase enzyme exhibits increased  
 CC levels of apparent expression which leads to an increased rate of  
 CC production of 2-keto-L-gluconic acid. The present amino acid sequence  
 CC represent the cassette mutagenesis wild-type pATP003.xb restriction site

CC peptide #3. This sequence was used in the methods of the invention for  
CC cassette mutagenesis.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

#### RESULT 49

AAU80624

ID AAU80624 standard; peptide; 7 AA.

XX

AC AAU80624;

XX

DT 26-MAR-2002 (first entry)

XX

DE Javelin peptide #54 for conjugation to multi-component viral particles.

XX

KW Immunogenic complex; non-pathogenic multi-component viral particle;  
KW javelin; heat shock protein; humoral immunity; cellular immunity;  
KW anti-viral immune response; viral infection; hepatitis; influenza;  
KW mumps; HIV infection; human immunodeficiency virus; polio;  
KW tick-borne encephalitis; ebola virus infection.

XX

OS Synthetic.

XX

PN WO200178772-A1.

XX

PD 25-OCT-2001.

XX

PF 17-APR-2001; 2001WO-US12568.

XX

PR 17-APR-2000; 2000US-197462P.

XX

PA (MOJA-) MOJAVE THERAPEUTICS INC.

XX

PI Hoe M, Landsberger F;

XX

DR WPI; 2002-049177/06.

XX

PT New heat shock protein-based viral vaccines, useful for enhancing  
PT anti-viral immune response in an organism, particularly as a vaccine  
PT for preventing or ameliorating viral infections, e.g. hepatitis,  
PT influenza or HIV infection -

XX

PS Disclosure; Page 11; 75pp; English.

XX

CC The present invention relates to the use of an immunogenic complex,  
CC comprising a non-pathogenic multi-component viral particle covalently  
CC linked to a javelin molecule (preferably a peptide) that selectively  
CC binds to a heat shock protein. The immunogenic complex is useful for

CC inducing both humoral and cellular immunity, especially for enhancing  
CC the anti-viral immune response, in a human or non-human subject. The  
CC immunogenic complex is particularly useful as a vaccine for preventing  
CC or ameliorating viral infections, e.g. hepatitis, influenza, mumps,  
CC HIV (human immunodeficiency virus) infection, polio, tick-borne  
CC encephalitis or ebola virus infection. AAU80571-AAU80734 represent  
CC javelin peptides which may be covalently conjugated to multi-component  
CC viral particles.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4

|||

Db 4 VLR 6

#### RESULT 50

AAU80668

ID AAU80668 standard; peptide; 7 AA.

XX

AC AAU80668;

XX

DT 26-MAR-2002 (first entry)

XX

DE Javelin peptide #98 for conjugation to multi-component viral particles.

XX

KW Immunogenic complex; non-pathogenic multi-component viral particle;

KW javelin; heat shock protein; humoral immunity; cellular immunity;

KW anti-viral immune response; viral infection; hepatitis; influenza;

KW mumps; HIV infection; human immunodeficiency virus; polio;

KW tick-borne encephalitis; ebola virus infection.

XX

OS Synthetic.

XX

PN WO200178772-A1.

XX

PD 25-OCT-2001.

XX

PF 17-APR-2001; 2001WO-US12568.

XX

PR 17-APR-2000; 2000US-197462P.

XX

PA (MOJA-) MOJAVE THERAPEUTICS INC.

XX

PI Hoe M, Landsberger F;

XX

DR WPI; 2002-049177/06.

XX

PT New heat shock protein-based viral vaccines, useful for enhancing

PT anti-viral immune response in an organism, particularly as a vaccine

PT for preventing or ameliorating viral infections, e.g. hepatitis,

PT influenza or HIV infection -

XX

PS Disclosure; Page 12; 75pp; English.

XX

CC The present invention relates to the use of an immunogenic complex,  
CC comprising a non-pathogenic multi-component viral particle covalently  
CC linked to a javelin molecule (preferably a peptide) that selectively  
CC binds to a heat shock protein. The immunogenic complex is useful for  
CC inducing both humoral and cellular immunity, especially for enhancing  
CC the anti-viral immune response, in a human or non-human subject. The  
CC immunogenic complex is particularly useful as a vaccine for preventing  
CC or ameliorating viral infections, e.g. hepatitis, influenza, mumps,  
CC HIV (human immunodeficiency virus) infection, polio, tick-borne  
CC encephalitis or ebola virus infection. AAU80571-AAU80734 represent  
CC javelin peptides which may be covalently conjugated to multi-component  
CC viral particles.

XX

SQ Sequence 7 AA;

Query Match 60.0%; Score 3; DB 23; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4

|||

Db 5 VLR 7

Search completed: November 28, 2003, 15:40:44

Job time : 43 secs

OM protein - protein search, using sw model

Run on: November 28, 2003, 15:39:25 ; Search time 22 Seconds  
 (without alignments)  
 9.616 Million cell updates/sec

Title: US-09-228-866-46  
 Perfect score: 5  
 Sequence: 1 XVLRX 5

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 175511

Minimum DB seq length: 5

Maximum DB seq length: 33

Post-processing: Listing first 100 summaries

Database : Issued\_Patents\_AA:\*  
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 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3	60.0	5	1	US-08-036-555B-165	Sequence 165, App
2	3	60.0	5	1	US-08-469-569-165	Sequence 165, App
3	3	60.0	5	1	US-08-249-322A-165	Sequence 165, App
4	3	60.0	5	1	US-08-469-526A-165	Sequence 165, App
5	3	60.0	5	2	US-08-734-591A-165	Sequence 165, App
6	3	60.0	5	2	US-08-469-660-165	Sequence 165, App
7	3	60.0	5	2	US-08-850-910A-13	Sequence 13, Appl
8	3	60.0	5	2	US-08-850-910A-49	Sequence 49, Appl
9	3	60.0	5	2	US-08-484-905-122	Sequence 122, App
10	3	60.0	5	3	US-08-481-985B-122	Sequence 122, App
11	3	60.0	5	3	US-08-954-915A-41	Sequence 41, Appl



12	3	60.0	5	3	US-08-470-335-165	Sequence 165, App
13	3	60.0	5	3	US-08-370-476-122	Sequence 122, App
14	3	60.0	5	3	US-08-735-021-165	Sequence 165, App
15	3	60.0	5	3	US-08-734-664A-165	Sequence 165, App
16	3	60.0	5	3	US-08-470-339-165	Sequence 165, App
17	3	60.0	5	4	US-09-463-129B-4	Sequence 4, Appli
18	3	60.0	5	4	US-08-467-602-165	Sequence 165, App
19	3	60.0	5	5	PCT-US94-05083C-161	Sequence 161, App
20	3	60.0	5	5	PCT-US95-06846A-165	Sequence 165, App
21	3	60.0	6	2	US-08-850-910A-14	Sequence 14, Appl
22	3	60.0	6	2	US-08-850-910A-16	Sequence 16, Appl
23	3	60.0	6	2	US-08-850-910A-50	Sequence 50, Appl
24	3	60.0	6	2	US-08-482-228-179	Sequence 179, App
25	3	60.0	6	3	US-08-482-528-179	Sequence 179, App
26	3	60.0	6	3	US-08-954-915A-33	Sequence 33, Appl
27	3	60.0	6	6	5314995-3	Patent No. 5314995
28	3	60.0	7	2	US-08-637-759B-124	Sequence 124, App
29	3	60.0	7	3	US-08-871-355A-124	Sequence 124, App
30	3	60.0	7	3	US-08-954-915A-42	Sequence 42, Appl
31	3	60.0	7	4	US-09-201-945-124	Sequence 124, App
32	3	60.0	7	4	US-09-658-645A-9	Sequence 9, Appli
33	3	60.0	8	1	US-08-526-710-4	Sequence 4, Appli
34	3	60.0	8	1	US-08-446-038B-11	Sequence 11, Appl
35	3	60.0	8	1	US-08-446-010B-11	Sequence 11, Appl
36	3	60.0	8	2	US-08-805-445-11	Sequence 11, Appl
37	3	60.0	8	2	US-08-064-067D-11	Sequence 11, Appl
38	3	60.0	8	2	US-09-066-208-11	Sequence 11, Appl
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41	3	60.0	8	4	US-09-227-906-4	Sequence 4, Appli
42	3	60.0	8	4	US-08-271-539-28	Sequence 28, Appl
43	3	60.0	8	4	US-08-271-539-29	Sequence 29, Appl
44	3	60.0	8	4	US-08-271-539-30	Sequence 30, Appl
45	3	60.0	8	4	US-08-271-539-31	Sequence 31, Appl
46	3	60.0	8	4	US-08-271-539-32	Sequence 32, Appl
47	3	60.0	8	4	US-09-555-313B-10	Sequence 10, Appl
48	3	60.0	8	5	PCT-US95-08354A-5	Sequence 5, Appli
49	3	60.0	9	1	US-08-526-710-20	Sequence 20, Appl
50	3	60.0	9	3	US-08-159-339A-272	Sequence 272, App
51	3	60.0	9	3	US-08-862-855-20	Sequence 20, Appl
52	3	60.0	9	3	US-08-787-091-3	Sequence 3, Appli
53	3	60.0	9	3	US-09-226-985-20	Sequence 20, Appl
54	3	60.0	9	4	US-09-227-906-20	Sequence 20, Appl
55	3	60.0	9	4	US-09-235-103-7	Sequence 7, Appli
56	3	60.0	10	1	US-08-125-746-5	Sequence 5, Appli
57	3	60.0	10	1	US-08-435-019-14	Sequence 14, Appl
58	3	60.0	10	1	US-08-435-019-15	Sequence 15, Appl
59	3	60.0	10	1	US-08-435-019-16	Sequence 16, Appl
60	3	60.0	10	2	US-08-622-720A-5	Sequence 5, Appli
61	3	60.0	10	2	US-08-406-330-13	Sequence 13, Appl
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63	3	60.0	10	2	US-08-556-597-13	Sequence 13, Appl
64	3	60.0	10	2	US-08-556-597-127	Sequence 127, App
65	3	60.0	10	2	US-08-637-899-7	Sequence 7, Appli
66	3	60.0	10	2	US-08-685-589A-102	Sequence 102, App
67	3	60.0	10	2	US-08-844-031-21	Sequence 21, Appl
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69	3	60.0	10	3	US-09-139-762A-87	Sequence 87, Appl
70	3	60.0	10	3	US-08-159-339A-286	Sequence 286, App
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72	3	60.0	10	3	US-09-188-579-60	Sequence 60, Appl
73	3	60.0	10	3	US-09-315-444-60	Sequence 60, Appl
74	3	60.0	10	4	US-09-721-362-60	Sequence 60, Appl
75	3	60.0	10	4	US-09-520-698-10	Sequence 10, Appl
76	3	60.0	11	1	US-08-217-188A-24	Sequence 24, Appl
77	3	60.0	11	1	US-08-687-226-24	Sequence 24, Appl
78	3	60.0	11	2	US-08-871-074-15	Sequence 15, Appl
79	3	60.0	11	3	US-08-667-725B-24	Sequence 24, Appl
80	3	60.0	11	3	US-08-526-136-19	Sequence 19, Appl
81	3	60.0	11	3	US-09-007-748-24	Sequence 24, Appl
82	3	60.0	11	4	US-08-469-260A-476	Sequence 476, App
83	3	60.0	11	4	US-08-488-446-476	Sequence 476, App
84	3	60.0	11	4	US-08-467-344A-476	Sequence 476, App
85	3	60.0	11	5	PCT-US94-05471-15	Sequence 15, Appl
86	3	60.0	12	1	US-07-778-233B-47	Sequence 47, Appl
87	3	60.0	12	1	US-07-963-321-47	Sequence 47, Appl
88	3	60.0	12	1	US-08-290-641-47	Sequence 47, Appl
89	3	60.0	12	1	US-08-548-540-47	Sequence 47, Appl
90	3	60.0	12	2	US-08-764-640-85	Sequence 85, Appl
91	3	60.0	12	3	US-08-973-225-85	Sequence 85, Appl
92	3	60.0	12	3	US-09-244-298A-85	Sequence 85, Appl
93	3	60.0	12	3	US-09-516-704-85	Sequence 85, Appl
94	3	60.0	12	3	US-09-461-697-439	Sequence 439, App
95	3	60.0	12	4	US-09-549-090-85	Sequence 85, Appl
96	3	60.0	12	4	US-09-832-230A-85	Sequence 85, Appl
97	3	60.0	12	5	PCT-US96-09809-47	Sequence 47, Appl
98	3	60.0	12	6	5164482-15	Patent No. 5164482
99	3	60.0	13	1	US-08-296-898-3	Sequence 3, Appli
100	3	60.0	13	1	US-08-435-019-10	Sequence 10, Appl

# ALIGNMENTS

## RESULT 1

US-08-036-555B-165

; Sequence 165, Application US/08036555B

; Patent No. 5530109

; GENERAL INFORMATION:

; APPLICANT: Goodearl, Andrew; Stroobant, Paul;

; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;

; APPLICANT: Chen, Maio Su; Hiles, Ian

; TITLE OF INVENTION: Glial Mitogenic Factors, Their

; TITLE OF INVENTION: Preparation and Use

; NUMBER OF SEQUENCES: 184

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

```

;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/036,555B
;      FILING DATE:  24-MAR-1993
;      CLASSIFICATION:  435
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/965,173
;      FILING DATE:  23-OCT-1992
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/940,389
;      FILING DATE:  03-SEP-1992
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/907,138
;      FILING DATE:  30-JUN-1992
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/863,703
;      FILING DATE:  03-APRIL-1992
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  U.K. 91 07566.3
;      FILING DATE:  10-APRIL-1991
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Tsai, Christine H.
;      REGISTRATION NUMBER:  34,266
;      REFERENCE/DOCKET NUMBER:  LUD 5250.4
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;      INFORMATION FOR SEQ ID NO:  165:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  5
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;      FEATURE:
;      OTHER INFORMATION:  Xaa in position 1 is unknown.
US-08-036-555B-165

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Query Match          60.0%;  Score 3;  DB 1;  Length 5;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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QY      2 VLR 4
      |||
Db      3 VLR 5

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## RESULT 2

US-08-469-569-165

; Sequence 165, Application US/08469569

; Patent No. 5606032

; GENERAL INFORMATION:

; APPLICANT: Goodearl, Andrew; Stroobant, Paul;

; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;

; APPLICANT: Chen, Maio Su; Hiles, Ian

; TITLE OF INVENTION: Glial Mitogenic Factors, Their

```

; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,569
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsai, Christine H.
; REGISTRATION NUMBER: 34,266
; REFERENCE/DOCKET NUMBER: LUD 5250.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-569-165

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Query Match          60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Db

|||  
3 VLR 5

RESULT 3

US-08-249-322A-165

; Sequence 165, Application US/08249322A

; Patent No. 5716930

; GENERAL INFORMATION:

; APPLICANT: Goodearl, Andrew; Stroobant, Paul;

; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;

; APPLICANT: Chen, Maio Su; Hiles, Ian

; TITLE OF INVENTION: Glial Mitogenic Factors, Their

; TITLE OF INVENTION: Preparation and Use

; NUMBER OF SEQUENCES: 184

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/249,322A

; FILING DATE: 26-MAY-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/036,555

; FILING DATE: 24-MAR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/965,173

; FILING DATE: 23-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/940,389

; FILING DATE: 03-SEP-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/907,138

; FILING DATE: 30-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/863,703

; FILING DATE: 03-APRIL-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.K. 91 07566.3

; FILING DATE: 10-APRIL-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Tsai, Christine H.

; REGISTRATION NUMBER: 34,266

; REFERENCE/DOCKET NUMBER: LUD 250.4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 165:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: Xaa in position 1 is unknown.  
US-08-249-322A-165

Query Match 60.0%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 4

US-08-469-526A-165  
; Sequence 165, Application US/08469526A  
; Patent No. 5792849  
; GENERAL INFORMATION:  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Stroobant, Paul  
; APPLICANT: Minghetti, Luisa  
; APPLICANT: Waterfield, Michael  
; APPLICANT: Marchionni, Mark  
; APPLICANT: Chen, Maio Su  
; APPLICANT: Hiles, Ian  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 187  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,526A  
; FILING DATE: 06 June 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/036,555  
; FILING DATE: 24-MAR-1993  
; APPLICATION NUMBER: 07/965,173  
; FILING DATE: 23-OCT-1992  
; APPLICATION NUMBER: 07/940,389  
; FILING DATE: 03-SEP-1992  
; APPLICATION NUMBER: 07/907,138

```

; FILING DATE: 03-JUN-1992
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-526A-165

```

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Query Match          60.0%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
        |||
Db      3 VLR 5

```

# RESULT 5

```

US-08-734-591A-165
; Sequence 165, Application US/08734591A
; Patent No. 5854220
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew
; APPLICANT: Stroobant, Paul
; APPLICANT: Minghetti, Luisa
; APPLICANT: Waterfield, Michael
; APPLICANT: Hiles, Ian
; APPLICANT: Marchionni, Mark
; APPLICANT: Chen, Mario
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 187
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible Pentium
; OPERATING SYSTEM: Windows95

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; SOFTWARE: WordPerfect (Version 7.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,591A
; FILING DATE: 22-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/470,335
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 03-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 91 07566.3
; FILING DATE: 10-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER: 39,109
; REFERENCE/DOCKET NUMBER: 04585/00200P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-734-591A-165

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Query Match          60.0%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      2 VLR 4
        |||
Db      3 VLR 5

```

```

RESULT 6
US-08-469-660-165
; Sequence 165, Application US/08469660
; Patent No. 5876973

```



```

; GENERAL INFORMATION:
;   APPLICANT: Gwynne, David I.; Marchionni, Mark;
;   APPLICANT: McBurney, Robert N.
;   TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
;   TITLE OF INVENTION: THEIR PREPARATION AND USE
;   NUMBER OF SEQUENCES: 184
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: Massachusetts
;     ZIP: 02111-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;     COMPUTER: IBM
;     OPERATING SYSTEM: PC-DOS
;     SOFTWARE: Wordperfect
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/469,660
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/011,396
;     FILING DATE: 29-JAN-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/984,085
;     FILING DATE: 01-DEC-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/951,747
;     FILING DATE: 25-SEP-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/927,337
;     FILING DATE: 10-AUG-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Clark, Paul T.
;     REGISTRATION NUMBER: 30,162
;     REFERENCE/DOCKET NUMBER: 04585/017004
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617) 542-5070
;     TELEFAX: 200154
;   INFORMATION FOR SEQ ID NO: 165:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 5
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
;     FEATURE:
;       OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-469-660-165

```

```

Query Match          60.0%; Score 3; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
      |||
Db      3 VLR 5

```

RESULT 7  
US-08-850-910A-13  
; Sequence 13, Application US/08850910A  
; Patent No. 5948761  
; GENERAL INFORMATION:  
; APPLICANT: SEILHAMER, J.J.  
; APPLICANT: LEWICKI, J.  
; APPLICANT: SCARBOROUGH, R.M.  
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR  
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER, LLP  
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/850,910A  
; FILING DATE: 05-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/477,226  
; FILING DATE: 08-FEB-1990  
; APPLICATION NUMBER: 07/299,880  
; FILING DATE: 19-JAN-1989  
; APPLICATION NUMBER: 07/206,470  
; FILING DATE: 14-JUN-1988  
; APPLICATION NUMBER: 07/200,383  
; FILING DATE: 31-MAY-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 219002025212  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-1500  
; TELEFAX: 202-822-0168  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Other  
; LOCATION: 1  
; OTHER INFORMATION: Amino Acid is Asn or Lys.

; NAME/KEY: Other  
; LOCATION: 5  
; OTHER INFORMATION: Amino Acid is Arg or Lys.  
US-08-850-910A-13

Query Match 60.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 8

US-08-850-910A-49

; Sequence 49, Application US/08850910A  
; Patent No. 5948761  
; GENERAL INFORMATION:  
; APPLICANT: SEILHAMER, J.J.  
; APPLICANT: LEWICKI, J.  
; APPLICANT: SCARBOROUGH, R.M.  
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR  
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER, LLP  
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/850,910A  
; FILING DATE: 05-MAY-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/477,226  
; FILING DATE: 08-FEB-1990  
; APPLICATION NUMBER: 07/299,880  
; FILING DATE: 19-JAN-1989  
; APPLICATION NUMBER: 07/206,470  
; FILING DATE: 14-JUN-1988  
; APPLICATION NUMBER: 07/200,383  
; FILING DATE: 31-MAY-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 219002025212  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-1500  
; TELEFAX: 202-822-0168

; TELEX:  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-850-910A-49

Query Match 60.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 9

US-08-484-905-122

; Sequence 122, Application US/08484905  
; Patent No. 5976551  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Philippe  
; TITLE OF INVENTION: An Altered Major Histocompatibility  
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the  
; TITLE OF INVENTION: Determinant  
; NUMBER OF SEQUENCES: 127  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS-/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,905  
; FILING DATE: 07-JUNE-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/801,818  
; FILING DATE: 05-DEC-1991  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/792,473  
; FILING DATE: 15-NOV-1991  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E. R.  
; REGISTRATION NUMBER: 33,332

; REFERENCE/DOCKET NUMBER: 03495.0106-03000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 122:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-484-905-122

Query Match 60.0%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 1 VLR 3

RESULT 10

US-08-481-985B-122

; Sequence 122, Application US/08481985B  
; Patent No. 6011146  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Phillipe  
; TITLE OF INVENTION: Altered Major Histocompatibility Complex  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 148  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481,985B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/801,818  
; FILING DATE: 05-DEC-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/792,473  
; FILING DATE: 15-NOV-1991  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.  
; REGISTRATION NUMBER: 25,146  
; REFERENCE/DOCKET NUMBER: 03495.0106-04000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 122:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-481-985B-122

Query Match 60.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 1 VLR 3

RESULT 11

US-08-954-915A-41

; Sequence 41, Application US/08954915A  
; Patent No. 6028055  
; GENERAL INFORMATION:  
; APPLICANT: Lowe, David  
; APPLICANT: Schoenfeld, Jill  
; TITLE OF INVENTION: Receptor Selective BNP  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/954,915A  
; FILING DATE: 21-Oct-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/028854  
; FILING DATE: 22-Oct-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.  
; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P1017R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8228

; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-954-915A-41

Query Match 60.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 12

US-08-470-335-165  
; Sequence 165, Application US/08470335F  
; Patent No. 6147190  
; GENERAL INFORMATION:  
; APPLICANT: GOODEARL, ANDREW  
; APPLICANT: STROOBANT, PAUL  
; APPLICANT: MINGHETTI, LUISA  
; APPLICANT: WATERFIELD, MICHAEL  
; APPLICANT: MARCHIONNI, MARK  
; APPLICANT: CHEN, MARIO S.  
; APPLICANT: HILES, IAN  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; FILE REFERENCE: 04585/00200B  
; CURRENT APPLICATION NUMBER: US/08/470,335F  
; CURRENT FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 08/036,555  
; EARLIER FILING DATE: 1993-03-24  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 165  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.  
US-08-470-335-165

Query Match 60.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 13  
 US-08-370-476-122  
 ; Sequence 122, Application US/08370476  
 ; Patent No. 6153408  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mottez, Estelle  
 ; APPLICANT: Abastado, Jean-Pierre  
 ; APPLICANT: Kourilsky, Phillipe  
 ; APPLICANT: Lone, Yu-Chun  
 ; APPLICANT: Ojcius, David  
 ; APPLICANT: Casrouge, Armanda  
 ; TITLE OF INVENTION: Altered Major Histocompatibility Complex  
 ; TITLE OF INVENTION:  
 ; NUMBER OF SEQUENCES: 127  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
 ; ADDRESSEE: Dunner  
 ; STREET: 1300 I Street, N.W., Suite 700  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; ZIP: 20005-3315  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/370,476  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/117,575  
 ; FILING DATE: 07-SEP-1993  
 ; APPLICATION NUMBER: US 08/072,787  
 ; FILING DATE: 06-JUN-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/801,818  
 ; FILING DATE: 05-DEC-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/792,473  
 ; FILING DATE: 15-NOV-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Meyers, Kenneth J.  
 ; REGISTRATION NUMBER: 25,146  
 ; REFERENCE/DOCKET NUMBER: 05243.0001-01000  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-408-4000  
 ; TELEFAX: 202-408-4400  
 ; INFORMATION FOR SEQ ID NO: 122:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-370-476-122

Query Match                      60.0%;   Score 3;   DB 3;   Length 5;



Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 1 VLR 3

RESULT 14

US-08-735-021-165  
; Sequence 165, Application US/08735021B  
; Patent No. 6194377  
; GENERAL INFORMATION:  
; APPLICANT: GOODEARL, ANDREW  
; APPLICANT: STROOBANT, PAUL  
; APPLICANT: MINGHETTI, LUISA  
; APPLICANT: WATERFIELD, MICHAEL  
; APPLICANT: MARCHIONNI, MARK  
; APPLICANT: CHEN, MARIO S.  
; APPLICANT: HILES, IAN  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; FILE REFERENCE: 04585/00200L  
; CURRENT APPLICATION NUMBER: US/08/735,021B  
; CURRENT FILING DATE: 1996-10-22  
; EARLIER APPLICATION NUMBER: 08/472,065  
; EARLIER FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 08/036,555  
; EARLIER FILING DATE: 1993-03-24  
; EARLIER APPLICATION NUMBER: 07/965,173  
; EARLIER FILING DATE: 1992-10-23  
; EARLIER APPLICATION NUMBER: 07/940,389  
; EARLIER FILING DATE: 1992-09-03  
; EARLIER APPLICATION NUMBER: 07/907,138  
; EARLIER FILING DATE: 1992-06-30  
; EARLIER APPLICATION NUMBER: 07/863,703  
; EARLIER FILING DATE: 1992-04-03  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 165  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: Xaa in 1 is unknown.  
US-08-735-021-165

Query Match 60.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 15  
US-08-734-664A-165  
; Sequence 165, Application US/08734664A  
; Patent No. 6204241  
; GENERAL INFORMATION:  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Stroobant, Paul  
; APPLICANT: Minghetti, Luisa  
; APPLICANT: Waterfield, Michael  
; APPLICANT: Marchionni, Mark  
; APPLICANT: Chen, Mario  
; APPLICANT: Hiles, Ian  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 187  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM Compatible Pentium  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/734,664A  
; FILING DATE: 22-OCT-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/249,322  
; FILING DATE: 26-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/036,555  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,173  
; FILING DATE: 23-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/940,389  
; FILING DATE: 03-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/907,138  
; FILING DATE: 30-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/863,703  
; FILING DATE: 03-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 91 07566.3  
; FILING DATE: 10-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bieker-Brady, Kristina  
; REGISTRATION NUMBER: 39,109  
; REFERENCE/DOCKET NUMBER: 04585/00200J

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 428-0200
; TELEFAX: (617) 428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
US-08-734-664A-165

```

```

Query Match          60.0%; Score 3; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

QY      2 VLR 4
        |||
Db      3 VLR 5

```

# RESULT 16

```

US-08-470-339-165
; Sequence 165, Application US/08470339C
; Patent No. 6232286
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROOBANT, PAUL
; APPLICANT: MINGHETTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 04585/002008
; CURRENT APPLICATION NUMBER: US/08/470,339C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; EARLIER APPLICATION NUMBER: 07/940,389
; EARLIER FILING DATE: 1992-09-03
; EARLIER APPLICATION NUMBER: 07/907,138
; EARLIER FILING DATE: 1992-06-30
; EARLIER APPLICATION NUMBER: 07/863,703
; EARLIER FILING DATE: 1992-04-03
; EARLIER APPLICATION NUMBER: 91 07566.3 GB
; EARLIER FILING DATE: 1999-04-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:

```

; NAME/KEY: VARIANT  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.  
US-08-470-339-165

Query Match 60.0%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 17

US-09-463-129B-4

; Sequence 4, Application US/09463129B  
; Patent No. 6410024  
; GENERAL INFORMATION:  
; APPLICANT: BURNIE, James P  
; APPLICANT: MATTHEWS, Ruth C  
; TITLE OF INVENTION: Epitopes of Shigella Like Toxin and Their Use as a  
; TITLE OF INVENTION: Vaccine and in Diagnosis  
; FILE REFERENCE: 264666  
; CURRENT APPLICATION NUMBER: US/09/463,129B  
; CURRENT FILING DATE: 2000-01-20  
; PRIOR APPLICATION NUMBER: GB 9715177.3  
; PRIOR FILING DATE: 1997-07-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/02156  
; PRIOR FILING DATE: 1998-07-17  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-09-463-129B-4

Query Match 60.0%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 18

US-08-467-602-165

; Sequence 165, Application US/08467602C  
; Patent No. 6444642  
; GENERAL INFORMATION:  
; APPLICANT: Sklar, Robert  
; APPLICANT: Marchionni, Mark  
; APPLICANT: Gwynne, David I.  
; TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND  
; TITLE OF INVENTION: DISORDERS

```

; FILE REFERENCE: 04585/028003
; CURRENT APPLICATION NUMBER: US/08/467,602C
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/209,204
; EARLIER FILING DATE: 1994-03-08
; EARLIER APPLICATION NUMBER: 08/059,022
; EARLIER FILING DATE: 1993-05-06
; NUMBER OF SEQ ID NOS: 420
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1)
; OTHER INFORMATION: Xaa in position 1 is Lys or Arg.
US-08-467-602-165

```

```

Query Match          60.0%; Score 3; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
        |||
Db      3 VLR 5

```

```

RESULT 19
PCT-US94-05083C-161
; Sequence 161, Application PC/TUS9405083C
; GENERAL INFORMATION:
; APPLICANT: Robert Sklar, Mark Marchionni,
; APPLICANT: David I. Gwynne
; TITLE OF INVENTION: METHODS FOR ALTERING
; TITLE OF INVENTION: MUSCLE CONDITION
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360
; MEDIUM TYPE: kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05083C
; FILING DATE: 06-MAY-94
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,204
; FILING DATE: 08-MAR-94
; PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER: 08/059,022
; FILING DATE: 06-May-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/028W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is
; OTHER INFORMATION: unknown.
PCT-US94-05083C-161

```

```

Query Match          60.0%; Score 3; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
      |||
Db      3 VLR 5

```

# RESULT 20

```

PCT-US95-06846A-165
; Sequence 165, Application PC/TUS9506846A
; GENERAL INFORMATION:
; APPLICANT: Goodearl, Andrew David; Stroobant, Paul;
; APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
; APPLICANT: Chen, Maio Su; Hiles, Ian
; TITLE OF INVENTION: Glial Mitogenic Factors, Their
; TITLE OF INVENTION: Preparation and Use
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06846A
; FILING DATE: 25-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/249,322

```

```

; FILING DATE: 26-MAY-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/036,555
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,173
; FILING DATE: 23-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/940,389
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/907,138
; FILING DATE: 30-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/863,703
; FILING DATE: 03-APRIL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.K. 91 07566.3
; FILING DATE: 10-APRIL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5250.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 165:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: Xaa in position 1 is unknown.
PCT-US95-06846A-165

```

```

Query Match          60.0%; Score 3; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
        |||
Db      3 VLR 5

```

```

RESULT 21
US-08-850-910A-14
; Sequence 14, Application US/08850910A
; Patent No. 5948761
; GENERAL INFORMATION:
; APPLICANT: SEILHAMER, J.J.
; APPLICANT: LEWICKI, J.
; APPLICANT: SCARBOROUGH, R.M.
; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE
; NUMBER OF SEQUENCES: 50

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER, LLP
; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/850,910A
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/477,226
; FILING DATE: 08-FEB-1990
; APPLICATION NUMBER: 07/299,880
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 07/206,470
; FILING DATE: 14-JUN-1988
; APPLICATION NUMBER: 07/200,383
; FILING DATE: 31-MAY-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 219002025212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1
; OTHER INFORMATION: Amino Acid is Asn or Lys.
; NAME/KEY: Other
; LOCATION: 5
; OTHER INFORMATION: Amino Acid is Arg or Lys.
; NAME/KEY: Other
; LOCATION: 6
; OTHER INFORMATION: Amino Acid is Tyr or His.
US-08-850-910A-14

```

```

Query Match          60.0%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```



Db

|||  
2 VLR 4

RESULT 22

US-08-850-910A-16

; Sequence 16, Application US/08850910A

; Patent No. 5948761

; GENERAL INFORMATION:

; APPLICANT: SEILHAMER, J.J.

; APPLICANT: LEWICKI, J.

; APPLICANT: SCARBOROUGH, R.M.

; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR

; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER, LLP

; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSEQ for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/850,910A

; FILING DATE: 05-MAY-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/477,226

; FILING DATE: 08-FEB-1990

; APPLICATION NUMBER: 07/299,880

; FILING DATE: 19-JAN-1989

; APPLICATION NUMBER: 07/206,470

; FILING DATE: 14-JUN-1988

; APPLICATION NUMBER: 07/200,383

; FILING DATE: 31-MAY-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Murashige, Kate H

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 219002025212

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-887-1500

; TELEFAX: 202-822-0168

; TELEX:

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-850-910A-16

Query Match 60.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 23

US-08-850-910A-50

; Sequence 50, Application US/08850910A

; Patent No. 5948761

; GENERAL INFORMATION:

; APPLICANT: SEILHAMER, J.J.

; APPLICANT: LEWICKI, J.

; APPLICANT: SCARBOROUGH, R.M.

; TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR

; TITLE OF INVENTION: PRODUCTION OF BRAIN NATRIUETIC PEPTIDE

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER, LLP

; STREET: 2000 Pennsylvania Avenue, NW, Suite 5500

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20006-1888

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSEQ for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/850,910A

; FILING DATE: 05-MAY-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/477,226

; FILING DATE: 08-FEB-1990

; APPLICATION NUMBER: 07/299,880

; FILING DATE: 19-JAN-1989

; APPLICATION NUMBER: 07/206,470

; FILING DATE: 14-JUN-1988

; APPLICATION NUMBER: 07/200,383

; FILING DATE: 31-MAY-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Murashige, Kate H

; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 219002025212

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-887-1500

; TELEFAX: 202-822-0168

; TELEX:

; INFORMATION FOR SEQ ID NO: 50:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6 amino acids

; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-850-910A-50

Query Match 60.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 24

US-08-482-228-179

; Sequence 179, Application US/08482228

; Patent No. 5968753

; GENERAL INFORMATION:

; APPLICANT: Tseng-Law, Janet

; APPLICANT: Kobori, Joan A.

; APPLICANT: Al-Abdaly, Fahad A.

; APPLICANT: Guillermo, Roy

; APPLICANT: Helgerson, Sam L.

; APPLICANT: Deans, Robert J.

; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL

; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE

; NUMBER OF SEQUENCES: 215

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Janice Guthrie, Ph.D.

; STREET: P.O. Box 15210

; CITY: Irvine

; STATE: California

; COUNTRY: USA

; ZIP: 92713-5210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/482,228

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Guthrie, Janice

; REGISTRATION NUMBER: 35,170

; REFERENCE/DOCKET NUMBER: IT-4630CIP3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (714) 440-5353

; TELEFAX: (714) 553-1952

; INFORMATION FOR SEQ ID NO: 179:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-482-228-179

Query Match 60.0%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 25

US-08-482-528-179

; Sequence 179, Application US/08482528  
; Patent No. 6017719  
; GENERAL INFORMATION:  
; APPLICANT: Tseng-Law, Janet  
; APPLICANT: Kobori, Joan A.  
; APPLICANT: Al-Abdaly, Fahad A.  
; APPLICANT: Guillermo, Roy  
; APPLICANT: Helgersen, Sam L.  
; APPLICANT: Deans, Robert J.  
; TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL  
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE  
; NUMBER OF SEQUENCES: 215  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Janice Guthrie, Ph.D.  
; STREET: P.O. Box 15210  
; CITY: Irvine  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92713-5210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,528  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Guthrie, Janice  
; REGISTRATION NUMBER: 35,170  
; REFERENCE/DOCKET NUMBER: IT-4630CIP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 440-5353  
; TELEFAX: (714) 553-1952  
; INFORMATION FOR SEQ ID NO: 179:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-482-528-179

Query Match 60.0%; Score 3; DB 3; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 26

US-08-954-915A-33

; Sequence 33, Application US/08954915A  
; Patent No. 6028055  
; GENERAL INFORMATION:  
; APPLICANT: Lowe, David  
; APPLICANT: Schoenfeld, Jill  
; TITLE OF INVENTION: Receptor Selective BNP  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/954,915A  
; FILING DATE: 21-Oct-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/028854  
; FILING DATE: 22-Oct-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.  
; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P1017R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8228  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-08-954-915A-33

Query Match 60.0%; Score 3; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 27  
 5314995-3  
 ; Patent No. 5314995  
 ; APPLICANT: FELL, HENRY P.; GAYLE, MARGIT A.  
 ; TITLE OF INVENTION: THERAPEUTIC INTERLEUKIN-2-ANTIBODY  
 ; BASED FUSION PROTEINS  
 ; NUMBER OF SEQUENCES: 8  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/468,390  
 ; FILING DATE: 22-JAN-1990  
 ; SEQ ID NO: 3:  
 ; LENGTH: 6  
 5314995-3

Query Match 60.0%; Score 3; DB 6; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 2 VLR 4

RESULT 28  
 US-08-637-759B-124  
 ; Sequence 124, Application US/08637759B  
 ; Patent No. 5876931  
 ; GENERAL INFORMATION:  
 ; APPLICANT: David William Holden  
 ; TITLE OF INVENTION: Identification of Genes  
 ; NUMBER OF SEQUENCES: 501  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Patrea L. Pabst  
 ; STREET: 2800 One Atlantic Center  
 ; STREET: 1201 West Peachtree Street  
 ; CITY: Atlanta  
 ; STATE: Georgia  
 ; COUNTRY: USA  
 ; ZIP: 30309-3450  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/637,759B  
 ; FILING DATE: 03-MAY-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/GB95/02875  
 ; FILING DATE: 11-DEC-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pabst, Patrea L.  
 ; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: RPMS 101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 124:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-637-759B-124

Query Match 60.0%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 29

US-08-871-355A-124  
; Sequence 124, Application US/08871355A  
; Patent No. 6015669  
; GENERAL INFORMATION:  
; APPLICANT: David William Holden  
; TITLE OF INVENTION: Identification of Genes  
; NUMBER OF SEQUENCES: 501  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/871,355A  
; FILING DATE: 09-JUN-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02875  
; FILING DATE: 11-DEC-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: RPMS 101 CON  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 124:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-871-355A-124

Query Match 60.0%; Score 3; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 30

US-08-954-915A-42

; Sequence 42, Application US/08954915A  
; Patent No. 6028055  
; GENERAL INFORMATION:  
; APPLICANT: Lowe, David  
; APPLICANT: Schoenfeld, Jill  
; TITLE OF INVENTION: Receptor Selective BNP  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/954,915A  
; FILING DATE: 21-Oct-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/028854  
; FILING DATE: 22-Oct-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kubinec, Jeffrey S.  
; REGISTRATION NUMBER: 36,575  
; REFERENCE/DOCKET NUMBER: P1017R1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8228  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 42:



; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-954-915A-42

Query Match 60.0%; Score 3; DB 3; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4

|||

Db 2 VLR 4

# RESULT 31

US-09-201-945-124

; Sequence 124, Application US/09201945

; Patent No. 6342215

; GENERAL INFORMATION:

; APPLICANT: David William Holden

; TITLE OF INVENTION: Identification of Genes

; NUMBER OF SEQUENCES: 501

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center

; STREET: 1201 West Peachtree Street

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/201,945

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/637,759

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: RPMS 101

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 873-8794

; TELEFAX: (404) 873-8795

; INFORMATION FOR SEQ ID NO: 124:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-09-201-945-124

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 32

US-09-658-645A-9  
; Sequence 9, Application US/09658645A  
; Patent No. 6423518  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Stephen  
; APPLICANT: Banta, Scott  
; TITLE OF INVENTION: Design and Production of Mutant 2,5-Diketo-D-gluconic  
; TITLE OF INVENTION: Acid Reductase Enzymes with Altered Cofactor Dependency  
; FILE REFERENCE: RU-0078  
; CURRENT APPLICATION NUMBER: US/09/658,645A  
; CURRENT FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-658-645A-9

Query Match 60.0%; Score 3; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 33

US-08-526-710-4  
; Sequence 4, Application US/08526710  
; Patent No. 5622699  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Method of Identifying Molecules That  
; TITLE OF INVENTION: Home to a Selected Organ In Vivo  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700

```

; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,710
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-526-710-4

```

```

Query Match          60.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
      |||
Db      2 VLR 4

```

#### RESULT 34

```

US-08-446-038B-11
; Sequence 11, Application US/08446038B
; Patent No. 5658791
; GENERAL INFORMATION:
; APPLICANT: Wilks, Andrew F.; Ziemiecki, Andrew;
; APPLICANT: Harpur, Ailsa
; TITLE OF INVENTION: No. 5658791el Protein Tyrosine Kinase
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS

```

```

; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,038B
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,067
; FILING DATE: 30-Jun-1993
; APPLICATION NUMBER: PCT/US91/08889
; FILING DATE: 26-No. 5658791-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Australian PK3594/90
; FILING DATE: 28-No. 5658791-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Australian 88229/91
; FILING DATE: 27-No. 5658791-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5658791man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5244
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-446-038B-11

```

```

Query Match          60.0%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
      |||
Db      4 VLR 6

```

```

RESULT 35
US-08-446-010B-11
; Sequence 11, Application US/08446010B
; Patent No. 5716818
; GENERAL INFORMATION:
; APPLICANT: Wilks, Andrew F.; Ziemiecki, Andrew;
; APPLICANT: Harpur, Ailsa
; TITLE OF INVENTION: No. 5716818e1 Protein Tyrosine Kinase
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

```

```

;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,010B
;      FILING DATE:  19-May-1995
;      CLASSIFICATION:  433
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/446,038
;      FILING DATE:  19-May-1995
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/064,067
;      FILING DATE:  30-Jun-1993
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/08889
;      FILING DATE:  26-No. 5716818-1991
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  Australian PK3594/90
;      FILING DATE:  28-No. 5716818-1990
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  Australian 88229/91
;      FILING DATE:  27-No. 5716818-1991
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Baer, Madeline F.
;      REGISTRATION NUMBER:  36,437
;      REFERENCE/DOCKET NUMBER:  LUD 5244.3
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-688-9200
;      TELEFAX:  212-838-3884
;      INFORMATION FOR SEQ ID NO:  11:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acid residues
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-446-010B-11

```

```

Query Match          60.0%;  Score 3;  DB 1;  Length 8;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 VLR 4
      |||
Db      4 VLR 6

```

```

RESULT 36
US-08-805-445-11
; Sequence 11, Application US/08805445
; Patent No. 5821069
; GENERAL INFORMATION:
; APPLICANT:  Wilks, Andrew F.; Ziemiecki, Andrew;
; APPLICANT:  Harpur, Ailsa
; TITLE OF INVENTION:  No. 5821069e1 Protein Tyrosine Kinase
; NUMBER OF SEQUENCES:  23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Felte & Lynch
; STREET:  805 Third Avenue

```

```

; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,445
; FILING DATE: 25-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,038
; FILING DATE: 19-MAY-1995
; APPLICATION NUMBER: 08/064,067
; FILING DATE: 30-Jun-1993
; APPLICATION NUMBER: PCT/US91/08889
; FILING DATE: 26-No. 5821069-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Australian PK3594/90
; FILING DATE: 28-No. 5821069-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: Australian 88229/91
; FILING DATE: 27-No. 5821069-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5821069man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5244
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
US-08-805-445-11

```

```

Query Match          60.0%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VLR 4
        |||
Db      4 VLR 6

```

```

RESULT 37
US-08-064-067D-11
; Sequence 11, Application US/08064067D
; Patent No. 5852184
; GENERAL INFORMATION:
; APPLICANT: Wilks, Andrew F.; Ziemiecki, Andrew;
; APPLICANT: Harpur, Ailsa
; TITLE OF INVENTION: No. 5852184el Protein Tyrosine Kinase

```

```

;   NUMBER OF SEQUENCES:  23
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Felfe & Lynch
;   STREET:  805 Third Avenue
;   CITY:  New York City
;   STATE:  New York
;   COUNTRY:  USA
;   ZIP:  10022
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;   COMPUTER:  IBM PS/2
;   OPERATING SYSTEM:  PC-DOS
;   SOFTWARE:  Wordperfect
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/064,067D
;   FILING DATE:  30-Jun-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US91/08889
;   FILING DATE:  26-No. 5852184-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  Australian PK3594/90
;   FILING DATE:  28-No. 5852184-1990
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  Australian 88229/91
;   FILING DATE:  27-No. 5852184-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Hanson, No. 5852184man D.
;   REGISTRATION NUMBER:  30,946
;   REFERENCE/DOCKET NUMBER:  LUD 5244
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  212-688-9200
;   TELEFAX:  212-838-3884
;   INFORMATION FOR SEQ ID NO:  11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  8 amino acid residues
;   TYPE:  amino acid
;   TOPOLOGY:  linear
US-08-064-067D-11

```

```

Query Match          60.0%;  Score 3;  DB 2;  Length 8;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 VLR 4
        |||
Db      4 VLR 6

```

```

RESULT 38
US-09-066-208-11
; Sequence 11, Application US/09066208
; Patent No. 5910426
; GENERAL INFORMATION:
; APPLICANT:  Wilks, Andrew F.; Ziemiecki, Andrew;
; APPLICANT:  Harpur, Ailsa
; TITLE OF INVENTION:  No. 5910426e1 Protein Tyrosine Kinase
; NUMBER OF SEQUENCES:  23

```

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Felfe & Lynch
;   STREET:  805 Third Avenue
;   CITY:  New York City
;   STATE:  New York
;   COUNTRY:  USA
;   ZIP:  10022
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette, 3.5 inch, 360 kb storage
;   COMPUTER:  IBM PS/2
;   OPERATING SYSTEM:  PC-DOS
;   SOFTWARE:  Wordperfect
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/066,208
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/805,445
;   FILING DATE:  25-FEB-1997
;   APPLICATION NUMBER:  US 08/446,038
;   FILING DATE:  19-MAY-1995
;   APPLICATION NUMBER:  08/064,067
;   FILING DATE:  30-Jun-1993
;   APPLICATION NUMBER:  PCT/US91/08889
;   FILING DATE:  26-No. 5910426-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  Australian PK3594/90
;   FILING DATE:  28-No. 5910426-1990
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  Australian 88229/91
;   FILING DATE:  27-No. 5910426-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Hanson, No. 5910426man D.
;   REGISTRATION NUMBER:  30,946
;   REFERENCE/DOCKET NUMBER:  LUD 5244
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  212-688-9200
;   TELEFAX:  212-838-3884
;   INFORMATION FOR SEQ ID NO:  11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  8 amino acid residues
;   TYPE:  amino acid
;   TOPOLOGY:  linear
US-09-066-208-11

```

```

Query Match          60.0%;  Score 3;  DB 2;  Length 8;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 VLR 4
        |||
Db      4 VLR 6

```

```

RESULT 39
US-08-862-855-4
; Sequence 4, Application US/08862855

```



; Patent No. 6068829  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Method of Identifying Molecules That  
; TITLE OF INVENTION: Home to a Selected Organ In Vivo  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/862,855  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/526,710  
; FILING DATE: 11-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/813,273  
; FILING DATE: 10-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 2621  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-862-855-4

Query Match 60.0%; Score 3; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 40  
US-09-226-985-4  
; Sequence 4, Application US/09226985  
; Patent No. 6296832

```

; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/226,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3423
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-226-985-4

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Query Match          60.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      2 VLR 4
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Db      2 VLR 4

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RESULT 41
US-09-227-906-4
; Sequence 4, Application US/09227906

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; Patent No. 6306365
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Method of Identifying Molecules That
; TITLE OF INVENTION: Home to a Selected Organ In Vivo
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,906
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,710
; FILING DATE: 11-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/813,273
; FILING DATE: 10-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,855
; FILING DATE: 23-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-227-906-4

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Query Match          60.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      2 VLR 4
      |||
Db      2 VLR 4

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RESULT 42

US-08-271-539-28

; Sequence 28, Application US/08271539  
; Patent No. 6358509  
; GENERAL INFORMATION:  
; APPLICANT: Ramanathan, Lata  
; APPLICANT: Seelig, Gail F.  
; APPLICANT: Trotta, Paul P.  
; TITLE OF INVENTION: Antibody Antagonists of Human Interleukin-4  
; FILE REFERENCE: JB0059KQ US  
; CURRENT APPLICATION NUMBER: US/08/271,539  
; CURRENT FILING DATE: 1994-07-07  
; PRIOR APPLICATION NUMBER: US 07/453,570  
; PRIOR FILING DATE: 1989-12-20  
; PRIOR APPLICATION NUMBER: PCT/US90/07289  
; PRIOR FILING DATE: 1990-12-18  
; PRIOR APPLICATION NUMBER: US 07/859,689  
; PRIOR FILING DATE: 1992-06-11  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: polypeptide

US-08-271-539-28

Query Match 60.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 43

US-08-271-539-29

; Sequence 29, Application US/08271539  
; Patent No. 6358509  
; GENERAL INFORMATION:  
; APPLICANT: Ramanathan, Lata  
; APPLICANT: Seelig, Gail F.  
; APPLICANT: Trotta, Paul P.  
; TITLE OF INVENTION: Antibody Antagonists of Human Interleukin-4  
; FILE REFERENCE: JB0059KQ US  
; CURRENT APPLICATION NUMBER: US/08/271,539  
; CURRENT FILING DATE: 1994-07-07  
; PRIOR APPLICATION NUMBER: US 07/453,570  
; PRIOR FILING DATE: 1989-12-20  
; PRIOR APPLICATION NUMBER: PCT/US90/07289  
; PRIOR FILING DATE: 1990-12-18  
; PRIOR APPLICATION NUMBER: US 07/859,689  
; PRIOR FILING DATE: 1992-06-11  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 29  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: polypeptide  
US-08-271-539-29

Query Match 60.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
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Db 4 VLR 6

RESULT 44

US-08-271-539-30

; Sequence 30, Application US/08271539  
; Patent No. 6358509  
; GENERAL INFORMATION:  
; APPLICANT: Ramanathan, Lata  
; APPLICANT: Seelig, Gail F.  
; APPLICANT: Trotta, Paul P.  
; TITLE OF INVENTION: Antibody Antagonists of Human Interleukin-4  
; FILE REFERENCE: JB0059KQ US  
; CURRENT APPLICATION NUMBER: US/08/271,539  
; CURRENT FILING DATE: 1994-07-07  
; PRIOR APPLICATION NUMBER: US 07/453,570  
; PRIOR FILING DATE: 1989-12-20  
; PRIOR APPLICATION NUMBER: PCT/US90/07289  
; PRIOR FILING DATE: 1990-12-18  
; PRIOR APPLICATION NUMBER: US 07/859,689  
; PRIOR FILING DATE: 1992-06-11  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: polypeptide  
US-08-271-539-30

Query Match 60.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 45

US-08-271-539-31

; Sequence 31, Application US/08271539  
; Patent No. 6358509  
; GENERAL INFORMATION:  
; APPLICANT: Ramanathan, Lata  
; APPLICANT: Seelig, Gail F.  
; APPLICANT: Trotta, Paul P.  
; TITLE OF INVENTION: Antibody Antagonists of Human Interleukin-4  
; FILE REFERENCE: JB0059KQ US  
; CURRENT APPLICATION NUMBER: US/08/271,539  
; CURRENT FILING DATE: 1994-07-07  
; PRIOR APPLICATION NUMBER: US 07/453,570  
; PRIOR FILING DATE: 1989-12-20  
; PRIOR APPLICATION NUMBER: PCT/US90/07289  
; PRIOR FILING DATE: 1990-12-18  
; PRIOR APPLICATION NUMBER: US 07/859,689  
; PRIOR FILING DATE: 1992-06-11  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: polypeptide

US-08-271-539-31

Query Match 60.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 46

US-08-271-539-32

; Sequence 32, Application US/08271539  
; Patent No. 6358509  
; GENERAL INFORMATION:  
; APPLICANT: Ramanathan, Lata  
; APPLICANT: Seelig, Gail F.  
; APPLICANT: Trotta, Paul P.  
; TITLE OF INVENTION: Antibody Antagonists of Human Interleukin-4  
; FILE REFERENCE: JB0059KQ US  
; CURRENT APPLICATION NUMBER: US/08/271,539  
; CURRENT FILING DATE: 1994-07-07  
; PRIOR APPLICATION NUMBER: US 07/453,570  
; PRIOR FILING DATE: 1989-12-20  
; PRIOR APPLICATION NUMBER: PCT/US90/07289  
; PRIOR FILING DATE: 1990-12-18  
; PRIOR APPLICATION NUMBER: US 07/859,689  
; PRIOR FILING DATE: 1992-06-11  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 32  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: polypeptide  
US-08-271-539-32

Query Match 60.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 1 VLR 3

RESULT 47

US-09-555-313B-10

; Sequence 10, Application US/09555313B  
; Patent No. 6506580  
; GENERAL INFORMATION:  
; APPLICANT: FICSHMEISTER, Rudolph et al.  
; TITLE OF INVENTION: Splicing variants of the human serotoninergic receptor  
; TITLE OF INVENTION: 5-HT4 and uses thereof, in particular for screening  
; FILE REFERENCE: P06762US00/BAS  
; CURRENT APPLICATION NUMBER: US/09/555,313B  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: FR 97/15037  
; PRIOR FILING DATE: 1997-11-28  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: OTHER  
; LOCATION: (2)..(2)  
; OTHER INFORMATION: Xaa in position 2 = aminohexanoic acid  
US-09-555-313B-10

Query Match 60.0%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 48

PCT-US95-08354A-5

; Sequence 5, Application PC/TUS9508354A  
; GENERAL INFORMATION:  
; APPLICANT: Temple University - Of The

```

; APPLICANT: Commonwealth System of Higher Education
; TITLE OF INVENTION: JAK3 PROTEIN TYROSINE
; TITLE OF INVENTION: KINASE AND DNA ENCODING THE SAME
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna
; ADDRESSEE: & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08354A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/272,368
; FILING DATE: 8 July 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-203 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
PCT-US95-08354A-5

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Query Match          60.0%; Score 3; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches    3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

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Qy      2 VLR 4
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Db      4 VLR 6

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#### RESULT 49

US-08-526-710-20

; Sequence 20, Application US/08526710

; Patent No. 5622699

; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki

; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: Method of Identifying Molecules That

; TITLE OF INVENTION: Home to a Selected Organ In Vivo



```

;   NUMBER OF SEQUENCES:  44
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Campbell and Flores
;       STREET:    4370 La Jolla Village Drive, Suite 700
;       CITY:      San Diego
;       STATE:     California
;       COUNTRY:   United States
;       ZIP:       92122
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:     IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/526,710
;       FILING DATE:       11-SEP-1995
;       CLASSIFICATION:    435
;   ATTORNEY/AGENT INFORMATION:
;       NAME:              Campbell, Cathryn A.
;       REGISTRATION NUMBER: 31,815
;       REFERENCE/DOCKET NUMBER:  P-LJ 1779
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE:        (619) 535-9001
;       TELEFAX:          (619) 535-8949
;   INFORMATION FOR SEQ ID NO: 20:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 9 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
US-08-526-710-20

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Query Match          60.0%;  Score 3;  DB 1;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 2.5e+05;
Matches   3;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy          2 VLR 4
            |||
Db          1 VLR 3

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# RESULT 50

US-08-159-339A-272

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; Sequence 272, Application US/08159339A
; Patent No. 6037135
;   GENERAL INFORMATION:
;       APPLICANT:  Kubo, Ralph T.
;       APPLICANT:  Grey, Howard M.
;       APPLICANT:  Sette, Alessandro
;       APPLICANT:  Celis, Esteban
;       TITLE OF INVENTION:  HLA Binding peptides and Their
;       TITLE OF INVENTION:  Uses
;       NUMBER OF SEQUENCES: 1254
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE:  Townsend and Townsend and Crew LLP
;           STREET:     Two Embarcadero Center, Eighth Floor
;           CITY:       San Francisco

```

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; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 272:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-272

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Query Match          60.0%; Score 3; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches    3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

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Qy      2 VLR 4
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Db      1 VLR 3

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Search completed: November 28, 2003, 15:42:38  
Job time : 24 secs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 28, 2003, 15:39:55 ; Search time 30 Seconds  
 (without alignments)  
 30.741 Million cell updates/sec

Title: US-09-228-866-46  
 Perfect score: 5  
 Sequence: 1 XVLRX 5

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 163174

Minimum DB seq length: 5  
 Maximum DB seq length: 33

Post-processing: Listing first 100 summaries

Database : Published\_Applications\_AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	ID	Description
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1	3	60.0	5	7	US-08-736-019-165	Sequence 165, App
2	3	60.0	5	11	US-09-902-517-13	Sequence 13, Appl
3	3	60.0	6	10	US-09-842-930A-46	Sequence 46, Appl
4	3	60.0	6	11	US-09-902-517-14	Sequence 14, Appl
5	3	60.0	6	11	US-09-902-517-16	Sequence 16, Appl
6	3	60.0	6	12	US-10-348-232-43	Sequence 43, Appl
7	3	60.0	7	11	US-09-954-385-384	Sequence 384, App
8	3	60.0	7	12	US-10-052-578-202	Sequence 202, App
9	3	60.0	7	12	US-10-052-578-246	Sequence 246, App
10	3	60.0	7	12	US-10-053-520-202	Sequence 202, App
11	3	60.0	7	12	US-10-053-520-246	Sequence 246, App
12	3	60.0	7	12	US-10-006-760-34	Sequence 34, Appl
13	3	60.0	7	12	US-10-053-498B-202	Sequence 202, App
14	3	60.0	7	12	US-10-053-498B-246	Sequence 246, App
15	3	60.0	7	15	US-10-273-541-55	Sequence 55, Appl
16	3	60.0	8	12	US-10-052-578-5	Sequence 5, Appli
17	3	60.0	8	12	US-10-283-423-53	Sequence 53, Appl
18	3	60.0	8	12	US-10-283-423-108	Sequence 108, App
19	3	60.0	8	12	US-10-283-423-111	Sequence 111, App
20	3	60.0	8	12	US-10-283-423-113	Sequence 113, App
21	3	60.0	8	12	US-10-283-423-122	Sequence 122, App
22	3	60.0	8	12	US-10-283-423-129	Sequence 129, App
23	3	60.0	8	12	US-10-053-520-5	Sequence 5, Appli
24	3	60.0	8	12	US-10-213-821-53	Sequence 53, Appl
25	3	60.0	8	12	US-10-213-821-108	Sequence 108, App
26	3	60.0	8	12	US-10-213-821-111	Sequence 111, App
27	3	60.0	8	12	US-10-213-821-113	Sequence 113, App
28	3	60.0	8	12	US-10-213-821-122	Sequence 122, App
29	3	60.0	8	12	US-10-213-821-129	Sequence 129, App
30	3	60.0	8	12	US-10-053-498B-5	Sequence 5, Appli
31	3	60.0	8	15	US-10-139-496-10	Sequence 10, Appl
32	3	60.0	9	9	US-09-760-599-42	Sequence 42, Appl
33	3	60.0	9	9	US-09-192-854-131	Sequence 131, App
34	3	60.0	9	10	US-09-780-053-338	Sequence 338, App
35	3	60.0	9	10	US-09-968-561A-234	Sequence 234, App
36	3	60.0	9	11	US-09-821-734-11	Sequence 11, Appl
37	3	60.0	9	11	US-09-809-638-29	Sequence 29, Appl
38	3	60.0	9	11	US-09-809-638-133	Sequence 133, App
39	3	60.0	9	11	US-09-809-638-231	Sequence 231, App
40	3	60.0	9	11	US-09-809-638-326	Sequence 326, App
41	3	60.0	9	11	US-09-809-638-524	Sequence 524, App
42	3	60.0	9	11	US-09-809-638-663	Sequence 663, App
43	3	60.0	9	11	US-09-978-309A-66	Sequence 66, Appl
44	3	60.0	9	12	US-10-141-645-93	Sequence 93, Appl
45	3	60.0	9	12	US-10-141-645-105	Sequence 105, App
46	3	60.0	9	12	US-10-141-645-112	Sequence 112, App
47	3	60.0	9	12	US-10-141-645-113	Sequence 113, App
48	3	60.0	9	12	US-10-141-645-118	Sequence 118, App
49	3	60.0	9	12	US-10-141-645-119	Sequence 119, App
50	3	60.0	9	12	US-09-968-744A-234	Sequence 234, App
51	3	60.0	9	12	US-10-283-423-109	Sequence 109, App
52	3	60.0	9	12	US-10-283-423-110	Sequence 110, App
53	3	60.0	9	12	US-10-283-423-123	Sequence 123, App
54	3	60.0	9	12	US-09-935-384-5	Sequence 5, Appli
55	3	60.0	9	12	US-09-935-384-37	Sequence 37, Appl
56	3	60.0	9	12	US-09-935-384-104	Sequence 104, App

57	3	60.0	9	12	US-09-935-384-246	Sequence 246, App
58	3	60.0	9	12	US-09-935-384-250	Sequence 250, App
59	3	60.0	9	12	US-09-935-384-311	Sequence 311, App
60	3	60.0	9	12	US-09-935-384-349	Sequence 349, App
61	3	60.0	9	12	US-09-935-384-515	Sequence 515, App
62	3	60.0	9	12	US-09-935-384-548	Sequence 548, App
63	3	60.0	9	12	US-09-935-384-620	Sequence 620, App
64	3	60.0	9	12	US-09-854-248-8	Sequence 8, Appli
65	3	60.0	9	12	US-10-306-878-12	Sequence 12, Appl
66	3	60.0	9	12	US-10-213-821-109	Sequence 109, App
67	3	60.0	9	12	US-10-213-821-110	Sequence 110, App
68	3	60.0	9	12	US-10-213-821-123	Sequence 123, App
69	3	60.0	9	15	US-10-281-478-34	Sequence 34, Appl
70	3	60.0	10	10	US-09-780-053-274	Sequence 274, App
71	3	60.0	10	10	US-09-780-053-691	Sequence 691, App
72	3	60.0	10	10	US-09-520-698-10	Sequence 10, Appl
73	3	60.0	10	10	US-09-842-930A-56	Sequence 56, Appl
74	3	60.0	10	11	US-09-809-638-79	Sequence 79, Appl
75	3	60.0	10	11	US-09-809-638-168	Sequence 168, App
76	3	60.0	10	11	US-09-809-638-209	Sequence 209, App
77	3	60.0	10	11	US-09-809-638-407	Sequence 407, App
78	3	60.0	10	11	US-09-809-638-411	Sequence 411, App
79	3	60.0	10	11	US-09-809-638-507	Sequence 507, App
80	3	60.0	10	11	US-09-809-638-574	Sequence 574, App
81	3	60.0	10	11	US-09-809-638-708	Sequence 708, App
82	3	60.0	10	11	US-09-572-404B-626	Sequence 626, App
83	3	60.0	10	11	US-09-572-404B-1164	Sequence 1164, Ap
84	3	60.0	10	11	US-09-572-404B-1908	Sequence 1908, Ap
85	3	60.0	10	11	US-09-572-404B-2455	Sequence 2455, Ap
86	3	60.0	10	11	US-09-572-404B-3858	Sequence 3858, Ap
87	3	60.0	10	11	US-09-572-404B-3859	Sequence 3859, Ap
88	3	60.0	10	12	US-09-572-270A-945	Sequence 945, App
89	3	60.0	10	12	US-10-229-368-78	Sequence 78, Appl
90	3	60.0	10	12	US-09-935-384-255	Sequence 255, App
91	3	60.0	10	12	US-09-935-384-287	Sequence 287, App
92	3	60.0	10	12	US-09-935-384-362	Sequence 362, App
93	3	60.0	10	12	US-09-935-384-495	Sequence 495, App
94	3	60.0	10	12	US-09-935-384-497	Sequence 497, App
95	3	60.0	10	12	US-09-935-384-655	Sequence 655, App
96	3	60.0	10	12	US-09-935-384-678	Sequence 678, App
97	3	60.0	10	12	US-09-573-822C-594	Sequence 594, App
98	3	60.0	10	15	US-10-116-255-40	Sequence 40, Appl
99	3	60.0	11	8	US-08-424-550B-476	Sequence 476, App
100	3	60.0	11	10	US-09-736-371B-29	Sequence 29, Appl

#### ALIGNMENTS

##### RESULT 1

US-08-736-019-165

; Sequence 165, Application US/08736019

; Publication No. US20030207799A1

; GENERAL INFORMATION:

; APPLICANT: Goodearl, Andrew

; APPLICANT: Stroobant, Paul

; APPLICANT: Minghetti, Luisa

; APPLICANT: Waterfield, Michael  
; APPLICANT: Marchionni, Mark  
; APPLICANT: Chen, Mario  
; APPLICANT: Hiles, Ian  
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR  
; TITLE OF INVENTION: PREPARATION AND USE  
; NUMBER OF SEQUENCES: 189  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM Compatible Pentium  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/736,019  
; FILING DATE: 22-OCT-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/471,833  
; FILING DATE: 06-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/036,555  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/965,173  
; FILING DATE: 23-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/907,138  
; FILING DATE: 30-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/940,389  
; FILING DATE: 03-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/863,703  
; FILING DATE: 03-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 91 07566.3  
; FILING DATE: 10-APR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bieker-Brady, Kristina  
; REGISTRATION NUMBER: 39,109  
; REFERENCE/DOCKET NUMBER: 04585/00200Q  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 428-0200  
; TELEFAX: (617) 428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 165:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5  
; TYPE: amino acid  
; STRANDEDNESS:

; TOPOLOGY: linear  
; FEATURE:  
; OTHER INFORMATION: Xaa in position 1 is unknown.  
US-08-736-019-165

Query Match 60.0%; Score 3; DB 7; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 3 VLR 5

RESULT 2

US-09-902-517-13

; Sequence 13, Application US/09902517  
; Publication No. US20030109430A1  
; GENERAL INFORMATION:  
; APPLICANT: Seilhamer, Jeffrey J.  
; APPLICANT: Lewicki, John  
; APPLICANT: Scarborough, Robert M.  
; APPLICANT: Porter, Gordon J.  
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN  
; TITLE OF INVENTION: NATRIURETIC PEPTIDE  
; FILE REFERENCE: 219002025213  
; CURRENT APPLICATION NUMBER: US/09/902,517  
; CURRENT FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 09/287,892  
; PRIOR FILING DATE: 1999-04-07  
; PRIOR APPLICATION NUMBER: 08/850,910  
; PRIOR FILING DATE: 1997-05-05  
; PRIOR APPLICATION NUMBER: 07/477,226  
; PRIOR FILING DATE: 1990-02-08  
; PRIOR APPLICATION NUMBER: 07/299,880  
; PRIOR FILING DATE: 1989-01-19  
; PRIOR APPLICATION NUMBER: 07/206,470  
; PRIOR FILING DATE: 1988-06-14  
; PRIOR APPLICATION NUMBER: 07/200,383  
; PRIOR FILING DATE: 1988-05-31  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: R2  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: Xaa = Asn or Lys  
; NAME/KEY: VARIANT  
; LOCATION: (5)...(5)  
; OTHER INFORMATION: Xaa = Arg or Lys  
US-09-902-517-13

Query Match 60.0%; Score 3; DB 11; Length 5;

Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 3

US-09-842-930A-46

; Sequence 46, Application US/09842930A  
; Publication No. US20020197681A1  
; GENERAL INFORMATION:  
; APPLICANT: Weigel, Paul  
; TITLE OF INVENTION: Identification of Hyaluronan Receptor for Endocytosis  
; FILE REFERENCE: 5820.603  
; CURRENT APPLICATION NUMBER: US/09/842,930A  
; CURRENT FILING DATE: 2001-04-22  
; PRIOR APPLICATION NUMBER: 60/245,320  
; PRIOR FILING DATE: 2000-11-02  
; PRIOR APPLICATION NUMBER: 60/199,538  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 46  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-842-930A-46

Query Match 60.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 4 VLR 6

RESULT 4

US-09-902-517-14

; Sequence 14, Application US/09902517  
; Publication No. US20030109430A1  
; GENERAL INFORMATION:  
; APPLICANT: Seilhamer, Jeffrey J.  
; APPLICANT: Lewicki, John  
; APPLICANT: Scarborough, Robert M.  
; APPLICANT: Porter, Gordon J.  
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN  
; TITLE OF INVENTION: NATRIURETIC PEPTIDE  
; FILE REFERENCE: 219002025213  
; CURRENT APPLICATION NUMBER: US/09/902,517  
; CURRENT FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 09/287,892  
; PRIOR FILING DATE: 1999-04-07  
; PRIOR APPLICATION NUMBER: 08/850,910  
; PRIOR FILING DATE: 1997-05-05



```

; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880
; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: R2
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: Xaa = Asn or Lys
;   NAME/KEY: VARIANT
;   LOCATION: (5)...(5)
;   OTHER INFORMATION: Xaa = Arg or Lys
;   NAME/KEY: VARIANT
;   LOCATION: (6)...(6)
;   OTHER INFORMATION: Xaa = Tyr or His
US-09-902-517-14

```

```

Query Match          60.0%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches    3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

QY          2 VLR 4
            |||
Db          2 VLR 4

```

# RESULT 5

```

US-09-902-517-16
; Sequence 16, Application US/09902517
; Publication No. US20030109430A1
; GENERAL INFORMATION:
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Lewicki, John
; APPLICANT: Scarborough, Robert M.
; APPLICANT: Porter, Gordon J.
; TITLE OF INVENTION: IMMUNOASSAYS FOR HUMAN AND CANINE BRAIN
; TITLE OF INVENTION: NATRIURETIC PEPTIDE
; FILE REFERENCE: 219002025213
; CURRENT APPLICATION NUMBER: US/09/902,517
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 09/287,892
; PRIOR FILING DATE: 1999-04-07
; PRIOR APPLICATION NUMBER: 08/850,910
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: 07/477,226
; PRIOR FILING DATE: 1990-02-08
; PRIOR APPLICATION NUMBER: 07/299,880

```

```

; PRIOR FILING DATE: 1989-01-19
; PRIOR APPLICATION NUMBER: 07/206,470
; PRIOR FILING DATE: 1988-06-14
; PRIOR APPLICATION NUMBER: 07/200,383
; PRIOR FILING DATE: 1988-05-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Proviso formula (1)
US-09-902-517-16

```

```

Query Match          60.0%; Score 3; DB 11; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
        |||
Db      2 VLR 4

```

```

RESULT 6
US-10-348-232-43
; Sequence 43, Application US/10348232
; Publication No. US20030186329A1
; GENERAL INFORMATION:
; APPLICANT: Madison, Edwin L.
; APPLICANT: Ke, Song-Hua
; TITLE OF INVENTION: USE OF SUBSTRATE SUBTRACTION LIBRARIES TO DISTINGUISH
; TITLE OF INVENTION: ENZYME SPECIFICITIES
; FILE REFERENCE: TSRI 543.1C1
; CURRENT APPLICATION NUMBER: US/10/348,232
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US 09/202,265
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PCT/US97/09760
; PRIOR FILING DATE: 1997-06-10
; PRIOR APPLICATION NUMBER: US 60/019,495
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-348-232-43

```

```

Query Match          60.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
        |||
Db      2 VLR 4

```

RESULT 7

US-09-954-385-384

; Sequence 384, Application US/09954385  
 ; Publication No. US20030100467A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aehle, Wolfgang  
 ; APPLICANT: Baldwin, Toby L.  
 ; APPLICANT: Van Gastel, Franciscus J.C.  
 ; APPLICANT: Janssen, Giselle G.  
 ; APPLICANT: Murray, Christopher J.  
 ; APPLICANT: Wang, Huaming  
 ; APPLICANT: Winetzky, Deborah S.  
 ; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide  
 ; TITLE OF INVENTION: Complexes  
 ; FILE REFERENCE: GC690  
 ; CURRENT APPLICATION NUMBER: US/09/954,385  
 ; CURRENT FILING DATE: 2001-09-12  
 ; NUMBER OF SEQ ID NOS: 433  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 384  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: binding peptide

US-09-954-385-384

Query Match 60.0%; Score 3; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 5 VLR 7

RESULT 8

US-10-052-578-202

; Sequence 202, Application US/10052578  
 ; Publication No. US20030134787A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sloan-Kettering Institute for Cancer Research  
 ; APPLICANT: Rothman, James E.  
 ; APPLICANT: Mayhew, Mark  
 ; APPLICANT: Hoe, Mee H.  
 ; APPLICANT: Houghton, Alan  
 ; APPLICANT: Hartl, Ulrich  
 ; APPLICANT: Ouerfelli, Ouathék  
 ; APPLICANT: Moroi, Yoichi  
 ; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
 ; FILE REFERENCE: 11746/46003  
 ; CURRENT APPLICATION NUMBER: US/10/052,578  
 ; CURRENT FILING DATE: 2002-01-17  
 ; PRIOR APPLICATION NUMBER: 08/961,707  
 ; PRIOR FILING DATE: 1997-10-31

; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 202  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-052-578-202

Query Match 60.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 4 VLR 6

RESULT 9

US-10-052-578-246  
; Sequence 246, Application US/10052578  
; Publication No. US20030134787A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Ouerfelli, Ouathak  
; APPLICANT: Moroi, Yoichi  
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES  
; FILE REFERENCE: 11746/46003  
; CURRENT APPLICATION NUMBER: US/10/052,578  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 08/961,707  
; PRIOR FILING DATE: 1997-10-31  
; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 246  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-052-578-246

Query Match 60.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 10

US-10-053-520-202

```
; Sequence 202, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 202
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-202
```

```
Query Match          60.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      2 VLR 4
      |||
Db      4 VLR 6
```

RESULT 11

US-10-053-520-246

```
; Sequence 246, Application US/10053520
; Publication No. US20030166530A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
```

; NUMBER OF SEQ ID NOS: 321  
; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 246  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in ml3 coliphage  
US-10-053-520-246

Query Match 60.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 12  
US-10-006-760-34  
; Sequence 34, Application US/10006760  
; Publication No. US20030186385A1  
; GENERAL INFORMATION:  
; APPLICANT: Koide, Shohei  
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND  
; TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF  
; FILE REFERENCE: 176/60901  
; CURRENT APPLICATION NUMBER: US/10/006,760  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/249,756  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AB loop  
; OTHER INFORMATION: sequence for polypeptide monobody in pYT45AB7N  
; OTHER INFORMATION: library  
US-10-006-760-34

Query Match 60.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 4 VLR 6

RESULT 13  
US-10-053-498B-202  
; Sequence 202, Application US/10053498B  
; Publication No. US20030194409A1

```
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathék
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 202
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-053-498B-202
```

```
Query Match          60.0%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      2 VLR 4
        |||
Db      4 VLR 6
```

# RESULT 14

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US-10-053-498B-246
; Sequence 246, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathék
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 246
; LENGTH: 7
```

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-053-498B-246

Query Match 60.0%; Score 3; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 15

US-10-273-541-55  
; Sequence 55, Application US/10273541  
; Publication No. US20030077277A1  
; GENERAL INFORMATION:  
; APPLICANT: Bayer Corporation  
; APPLICANT: Takeuchi, Toshi  
; TITLE OF INVENTION: Human Antibodies That Have MN Binding and Cell Adhesion-  
Neutralizing  
; TITLE OF INVENTION: Activity  
; FILE REFERENCE: MSB-7289  
; CURRENT APPLICATION NUMBER: US/10/273,541  
; CURRENT FILING DATE: 2002-10-18  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-273-541-55

Query Match 60.0%; Score 3; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

RESULT 16

US-10-052-578-5  
; Sequence 5, Application US/10052578  
; Publication No. US20030134787A1  
; GENERAL INFORMATION:  
; APPLICANT: Sloan-Kettering Institute for Cancer Research  
; APPLICANT: Rothman, James E.  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee H.  
; APPLICANT: Houghton, Alan  
; APPLICANT: Hartl, Ulrich  
; APPLICANT: Ouerfelli, Ouathak



```

; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46003
; CURRENT APPLICATION NUMBER: US/10/052,578
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in m13 coliphage
US-10-052-578-5

```

```

Query Match          60.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
        |||
Db      5 VLR 7

```

# RESULT 17

US-10-283-423-53

```

; Sequence 53, Application US/10283423
; Publication No. US20030162223A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,
And Methods
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: PHRM0002-102
; Application Project
; -----
; CURRENT APPLICATION NUMBER: US/10/283,423
; CURRENT FILING DATE: 2002-10-30
; Earlier Applications
; -----
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
; PRIOR FILING DATE: PriorFilingDate : 2000-10-20
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
; PRIOR FILING DATE: PriorFilingDate : 1999-10-22
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030162223A1el Sequence

```

US-10-283-423-53

Query Match 60.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 18

US-10-283-423-108

; Sequence 108, Application US/10283423  
; Publication No. US20030162223A1  
; GENERAL INFORMATION:  
; APPLICANT: Lowery, David E.  
; APPLICANT: Smith, Valdin G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,  
And Methods  
; TITLE OF INVENTION: Related To The Same  
; FILE REFERENCE: PHRM0002-102  
; Application Project  
; -----  
; CURRENT APPLICATION NUMBER: US/10/283,423  
; CURRENT FILING DATE: 2002-10-30  
; Earlier Applications  
; -----  
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746  
; PRIOR FILING DATE: PriorFilingDate : 2000-10-20  
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676  
; PRIOR FILING DATE: PriorFilingDate : 1999-10-22  
; NUMBER OF SEQ ID NOS: 187  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 108  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. US20030162223A1el Sequence  
US-10-283-423-108

Query Match 60.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 19

US-10-283-423-111

; Sequence 111, Application US/10283423  
; Publication No. US20030162223A1

```

; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,
And Methods
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: PHRM0002-102
; Application Project
; -----
; CURRENT APPLICATION NUMBER: US/10/283,423
; CURRENT FILING DATE: 2002-10-30
; Earlier Applications
; -----
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
; PRIOR FILING DATE: PriorFilingDate : 2000-10-20
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
; PRIOR FILING DATE: PriorFilingDate : 1999-10-22
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 111
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030162223A1el Sequence
US-10-283-423-111

```

```

Query Match          60.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 VLR 4
      |||
Db      5 VLR 7

```

# RESULT 20

```

US-10-283-423-113
; Sequence 113, Application US/10283423
; Publication No. US20030162223A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,
And Methods
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: PHRM0002-102
; Application Project
; -----
; CURRENT APPLICATION NUMBER: US/10/283,423
; CURRENT FILING DATE: 2002-10-30
; Earlier Applications
; -----

```

```

; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
; PRIOR FILING DATE: PriorFilingDate : 2000-10-20
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
; PRIOR FILING DATE: PriorFilingDate : 1999-10-22
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 113
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. US20030162223A1el Sequence
US-10-283-423-113

```

```

Query Match          60.0%;  Score 3;  DB 12;  Length 8;
Best Local Similarity 100.0%;  Pred. No. 6e+05;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      2 VLR 4
        |||
Db      5 VLR 7

```

```

RESULT 21
US-10-283-423-122
; Sequence 122, Application US/10283423
; Publication No. US20030162223A1
; GENERAL INFORMATION:
;   APPLICANT: Lowery, David E.
;   APPLICANT: Smith, Valdin G.
;   APPLICANT: Kubiak, Teresa M.
;   APPLICANT: Larsen, Martha J.
;   TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,
And Methods
;   TITLE OF INVENTION: Related To The Same
;   FILE REFERENCE: PHRM0002-102
;   Application Project
;   -----
;   CURRENT APPLICATION NUMBER: US/10/283,423
;   CURRENT FILING DATE: 2002-10-30
;   Earlier Applications
;   -----
;   PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
;   PRIOR FILING DATE: PriorFilingDate : 2000-10-20
;   PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
;   PRIOR FILING DATE: PriorFilingDate : 1999-10-22
;   NUMBER OF SEQ ID NOS: 187
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 122
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: No. US20030162223A1el Sequence
US-10-283-423-122

```

```

Query Match          60.0%;  Score 3;  DB 12;  Length 8;

```

Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 22

US-10-283-423-129

; Sequence 129, Application US/10283423

; Publication No. US20030162223A1

; GENERAL INFORMATION:

; APPLICANT: Lowery, David E.

; APPLICANT: Smith, Valdin G.

; APPLICANT: Kubiak, Teresa M.

; APPLICANT: Larsen, Martha J.

; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,  
And Methods

; TITLE OF INVENTION: Related To The Same

; FILE REFERENCE: PHRM0002-102

; Application Project

; -----

; CURRENT APPLICATION NUMBER: US/10/283,423

; CURRENT FILING DATE: 2002-10-30

; Earlier Applications

; -----

; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746

; PRIOR FILING DATE: PriorFilingDate : 2000-10-20

; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676

; PRIOR FILING DATE: PriorFilingDate : 1999-10-22

; NUMBER OF SEQ ID NOS: 187

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 129

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: No. US20030162223A1el Sequence

US-10-283-423-129

Query Match 60.0%; Score 3; DB 12; Length 8;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 23

US-10-053-520-5

; Sequence 5, Application US/10053520

; Publication No. US20030166530A1

; GENERAL INFORMATION:

; APPLICANT: Sloan-Kettering Institute for Cancer Research

; APPLICANT: Rothman, James E.

```
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathek
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46004
; CURRENT APPLICATION NUMBER: US/10/053,520
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide in ml3 coliphage
US-10-053-520-5
```

```
Query Match          60.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
QY          2 VLR 4
            |||
Db          5 VLR 7
```

```
RESULT 24
US-10-213-821-53
; Sequence 53, Application US/10213821
; Publication No. US20030180297A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,
And Methods
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.2cp
; CURRENT APPLICATION NUMBER: US/10/213,821
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/693,746
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

; FEATURE:  
; OTHER INFORMATION: No. US20030180297A1e1 Sequence  
US-10-213-821-53

Query Match 60.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 25

US-10-213-821-108

; Sequence 108, Application US/10213821  
; Publication No. US20030180297A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia & Upjohn  
; APPLICANT: Lowery, David E.  
; APPLICANT: Smith, Valdin G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,  
And Methods  
; TITLE OF INVENTION: Related To The Same  
; FILE REFERENCE: 6297.2cp  
; CURRENT APPLICATION NUMBER: US/10/213,821  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 09/693,746  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/425,676  
; PRIOR FILING DATE: 1999-10-22  
; NUMBER OF SEQ ID NOS: 185  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 108  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. US20030180297A1e1 Sequence  
US-10-213-821-108

Query Match 60.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 26

US-10-213-821-111

; Sequence 111, Application US/10213821  
; Publication No. US20030180297A1  
; GENERAL INFORMATION:

```

; APPLICANT: Pharmacia & Upjohn
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,
And Methods
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.2cp
; CURRENT APPLICATION NUMBER: US/10/213,821
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/693,746
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 111
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030180297A1el Sequence
US-10-213-821-111

```

```

Query Match          60.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy          2 VLR 4
            |||
Db          5 VLR 7

```

```

RESULT 27
US-10-213-821-113
; Sequence 113, Application US/10213821
; Publication No. US20030180297A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,
And Methods
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.2cp
; CURRENT APPLICATION NUMBER: US/10/213,821
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/693,746
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113

```



; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. US20030180297A1el Sequence  
US-10-213-821-113

Query Match 60.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 28

US-10-213-821-122

; Sequence 122, Application US/10213821  
; Publication No. US20030180297A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia & Upjohn  
; APPLICANT: Lowery, David E.  
; APPLICANT: Smith, Valdin G.  
; APPLICANT: Kubiak, Teresa M.  
; APPLICANT: Larsen, Martha J.  
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,  
And Methods  
; TITLE OF INVENTION: Related To The Same  
; FILE REFERENCE: 6297.2cp  
; CURRENT APPLICATION NUMBER: US/10/213,821  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 09/693,746  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/425,676  
; PRIOR FILING DATE: 1999-10-22  
; NUMBER OF SEQ ID NOS: 185  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 122  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. US20030180297A1el Sequence  
US-10-213-821-122

Query Match 60.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 29

US-10-213-821-129

```

; Sequence 129, Application US/10213821
; Publication No. US20030180297A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids,
And Methods
; TITLE OF INVENTION: Related To The Same
; FILE REFERENCE: 6297.2cp
; CURRENT APPLICATION NUMBER: US/10/213,821
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 09/693,746
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US20030180297A1 Sequence
US-10-213-821-129

```

```

Query Match          60.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
      |||
Db      5 VLR 7

```

```

RESULT 30
US-10-053-498B-5
; Sequence 5, Application US/10053498B
; Publication No. US20030194409A1
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute for Cancer Research
; APPLICANT: Rothman, James E.
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Hartl, Ulrich
; APPLICANT: Ouerfelli, Ouathak
; APPLICANT: Moroi, Yoichi
; TITLE OF INVENTION: CONJUGATE HEAT SHOCK PROTEIN-BINDING PEPTIDES
; FILE REFERENCE: 11746/46002
; CURRENT APPLICATION NUMBER: US/10/053,498B
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 08/961,707
; PRIOR FILING DATE: 1997-10-31
; NUMBER OF SEQ ID NOS: 321

```

; SOFTWARE: WordPerfect 8.0 for Windows  
; SEQ ID NO 5  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptide in m13 coliphage  
US-10-053-498B-5

Query Match 60.0%; Score 3; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 31

US-10-139-496-10  
; Sequence 10, Application US/10139496  
; Publication No. US20030082646A1  
; GENERAL INFORMATION:  
; APPLICANT: Carey, Thomas E.  
; APPLICANT: Nair, Thankum S.  
; APPLICANT: Gray, Jennifer P.  
; TITLE OF INVENTION: Antigenic Targets of Autoimmune Sensorineural Hearing Loss (AISNHL) and  
; TITLE OF INVENTION: Development of Tests for Diagnosis and Management of AISNHL  
; FILE REFERENCE: UM-6982  
; CURRENT APPLICATION NUMBER: US/10/139,496  
; CURRENT FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: 09/222,179  
; PRIOR FILING DATE: 1998-12-29  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-139-496-10

Query Match 60.0%; Score 3; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 6 VLR 8

RESULT 32

US-09-760-599-42  
; Sequence 42, Application US/09760599

; Patent No. US20010034326A1  
; GENERAL INFORMATION:  
; APPLICANT: Larson Mr., Richard S.  
; TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction  
; FILE REFERENCE: SCI200/4-1CIP  
; CURRENT APPLICATION NUMBER: US/09/760,599  
; CURRENT FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
US-09-760-599-42

Query Match 60.0%; Score 3; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 2 VLR 4

#### RESULT 33

US-09-192-854-131  
; Sequence 131, Application US/09192854  
; Patent No. US20020068276A1  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Greg  
; APPLICANT: Tomlinson, Ian  
; TITLE OF INVENTION: Methods for Selecting Functional Peptides  
; FILE REFERENCE: 3789/72916  
; CURRENT APPLICATION NUMBER: US/09/192,854  
; CURRENT FILING DATE: 1998-11-17  
; EARLIER APPLICATION NUMBER: 60/066,729  
; EARLIER FILING DATE: 1997-11-21  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 131  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-192-854-131

Query Match 60.0%; Score 3; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 4 VLR 6

#### RESULT 34

US-09-780-053-338  
 ; Sequence 338, Application US/09780053  
 ; Patent No. US20020102640A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Elana Levin  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN  
 ; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER  
 ; FILE REFERENCE: 129.5USU1  
 ; CURRENT APPLICATION NUMBER: US/09/780,053  
 ; CURRENT FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/181,261  
 ; PRIOR FILING DATE: 2000-02-09  
 ; NUMBER OF SEQ ID NOS: 716  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 338  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 US-09-780-053-338

Query Match 60.0%; Score 3; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 7 VLR 9

RESULT 35  
 US-09-968-561A-234  
 ; Sequence 234, Application US/09968561A  
 ; Patent No. US20020164642A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tomlinson, Ian M  
 ; APPLICANT: Winter, Gregory  
 ; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different  
 Ligands  
 ; FILE REFERENCE: 8039/1073B  
 ; CURRENT APPLICATION NUMBER: US/09/968,561A  
 ; CURRENT FILING DATE: 2001-10-01  
 ; PRIOR APPLICATION NUMBER: GB 9722131.1  
 ; PRIOR FILING DATE: 1997-10-20  
 ; PRIOR APPLICATION NUMBER: US 60/065,248  
 ; PRIOR FILING DATE: 1997-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/066,729  
 ; PRIOR FILING DATE: 1997-11-21  
 ; PRIOR APPLICATION NUMBER: PCT/GB98/03135  
 ; PRIOR FILING DATE: 1998-10-20  
 ; PRIOR APPLICATION NUMBER: US 09/511,939  
 ; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 234  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-968-561A-234

Query Match 60.0%; Score 3; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
|||  
Db 4 VLR 6

RESULT 36

US-09-821-734-11  
; Sequence 11, Application US/09821734  
; Publication No. US20030027246A1  
; GENERAL INFORMATION:  
; APPLICANT: Chong, Pele  
; APPLICANT: Pedyczak, Artur  
; APPLICANT: Sia, Charles Dwo Yuan  
; TITLE OF INVENTION: Immunogenic Peptides Derived from Prostate-Specific  
Membrane Antigen  
; TITLE OF INVENTION: (PSMA) and Uses Thereof  
; FILE REFERENCE: 11014-22  
; CURRENT APPLICATION NUMBER: US/09/821,734  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193,386  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 11  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: CLP335  
US-09-821-734-11

Query Match 60.0%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
|||  
Db 1 VLR 3

RESULT 37

US-09-809-638-29  
; Sequence 29, Application US/09809638  
; Publication No. US20030059895A1  
; GENERAL INFORMATION:

; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.35US01  
; CURRENT APPLICATION NUMBER: US/09/809,638  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 746  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-638-29

Query Match 60.0%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 4 VLR 6

RESULT 38  
US-09-809-638-133  
; Sequence 133, Application US/09809638  
; Publication No. US20030059895A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.35US01  
; CURRENT APPLICATION NUMBER: US/09/809,638  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 746  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 133  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-638-133

Query Match 60.0%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4

Db                    |||  
                      3 VLR 5

RESULT 39

US-09-809-638-231  
; Sequence 231, Application US/09809638  
; Publication No. US20030059895A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.35US01  
; CURRENT APPLICATION NUMBER: US/09/809,638  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 746  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 231  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-638-231

Query Match                    60.0%; Score 3; DB 11; Length 9;  
Best Local Similarity       100.0%; Pred. No. 6e+05;  
Matches       3; Conservative       0; Mismatches       0; Indels       0; Gaps       0;

Qy                    2 VLR 4  
                      |||  
Db                    4 VLR 6

RESULT 40

US-09-809-638-326  
; Sequence 326, Application US/09809638  
; Publication No. US20030059895A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.35US01  
; CURRENT APPLICATION NUMBER: US/09/809,638  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 746  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 326  
; LENGTH: 9



; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-638-326

Query Match 60.0%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 7 VLR 9

RESULT 41

US-09-809-638-524

; Sequence 524, Application US/09809638  
; Publication No. US20030059895A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.35US01  
; CURRENT APPLICATION NUMBER: US/09/809,638  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 746  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 524  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-638-524

Query Match 60.0%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 1 VLR 3

RESULT 42

US-09-809-638-663

; Sequence 663, Application US/09809638  
; Publication No. US20030059895A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Faris  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Aya Jakobovits

; TITLE OF INVENTION: 125P5C8: A TISSUE SPECIFIC PROTEIN  
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.35US01  
; CURRENT APPLICATION NUMBER: US/09/809,638  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 746  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 663  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-638-663

Query Match 60.0%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 1 VLR 3

RESULT 43

US-09-978-309A-66  
; Sequence 66, Application US/09978309A  
; Publication No. US20030100490A1  
; GENERAL INFORMATION:  
; APPLICANT: Cruz, Tony  
; APPLICANT: Pastrak, Aleksandra  
; APPLICANT: Turley, Eva A.  
; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response  
to  
; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated  
by  
; TITLE OF INVENTION: Hyaladherin and Hyaluronans  
; FILE REFERENCE: 033352-010  
; CURRENT APPLICATION NUMBER: US/09/978,309A  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: US 09/685,010  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: US 09/541,522  
; PRIOR FILING DATE: 2000-04-03  
; PRIOR APPLICATION NUMBER: US 60/127,457  
; PRIOR FILING DATE: 1999-04-01  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 66  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-978-309A-66

Query Match 60.0%; Score 3; DB 11; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4

Db

|||  
7 VLR 9

RESULT 44

US-10-141-645-93

; Sequence 93, Application US/10141645  
; Publication No. US20030144184A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert Lehrer  
; APPLICANT: Alan Waring  
; APPLICANT: Alexander Cole  
; APPLICANT: Teresa Hong  
; TITLE OF INVENTION: Retrocyclins - Antiviral and  
; TITLE OF INVENTION: Antimicrobial Peptides  
; FILE REFERENCE: UCLA-001CIP  
; CURRENT APPLICATION NUMBER: US/10/141,645  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/284,855  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: Unassigned  
; PRIOR FILING DATE: 2002-04-18  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 93  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: expansion of variant residues.

US-10-141-645-93

Query Match 60.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4

|||  
Db 5 VLR 7

RESULT 45

US-10-141-645-105

; Sequence 105, Application US/10141645  
; Publication No. US20030144184A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert Lehrer  
; APPLICANT: Alan Waring  
; APPLICANT: Alexander Cole  
; APPLICANT: Teresa Hong  
; TITLE OF INVENTION: Retrocyclins - Antiviral and  
; TITLE OF INVENTION: Antimicrobial Peptides  
; FILE REFERENCE: UCLA-001CIP  
; CURRENT APPLICATION NUMBER: US/10/141,645  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/284,855  
; PRIOR FILING DATE: 2001-04-18

; PRIOR APPLICATION NUMBER: Unassigned  
; PRIOR FILING DATE: 2002-04-18  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 105  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: expansion of variant residues.  
US-10-141-645-105

Query Match 60.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 46  
US-10-141-645-112  
; Sequence 112, Application US/10141645  
; Publication No. US20030144184A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert Lehrer  
; APPLICANT: Alan Waring  
; APPLICANT: Alexander Cole  
; APPLICANT: Teresa Hong  
; TITLE OF INVENTION: Retrocyclins - Antiviral and  
; TITLE OF INVENTION: Antimicrobial Peptides  
; FILE REFERENCE: UCLA-001CIP  
; CURRENT APPLICATION NUMBER: US/10/141,645  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/284,855  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: Unassigned  
; PRIOR FILING DATE: 2002-04-18  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 112  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: expansion of variant residues.  
US-10-141-645-112

Query Match 60.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 47

US-10-141-645-113

; Sequence 113, Application US/10141645  
 ; Publication No. US20030144184A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert Lehrer  
 ; APPLICANT: Alan Waring  
 ; APPLICANT: Alexander Cole  
 ; APPLICANT: Teresa Hong  
 ; TITLE OF INVENTION: Retrocyclins - Antiviral and  
 ; TITLE OF INVENTION: Antimicrobial Peptides  
 ; FILE REFERENCE: UCLA-001CIP  
 ; CURRENT APPLICATION NUMBER: US/10/141,645  
 ; CURRENT FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: 60/284,855  
 ; PRIOR FILING DATE: 2001-04-18  
 ; PRIOR APPLICATION NUMBER: Unassigned  
 ; PRIOR FILING DATE: 2002-04-18  
 ; NUMBER OF SEQ ID NOS: 125  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 113  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: expansion of variant residues.

US-10-141-645-113

Query Match 60.0%; Score 3; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 5 VLR 7

RESULT 48

US-10-141-645-118

; Sequence 118, Application US/10141645  
 ; Publication No. US20030144184A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert Lehrer  
 ; APPLICANT: Alan Waring  
 ; APPLICANT: Alexander Cole  
 ; APPLICANT: Teresa Hong  
 ; TITLE OF INVENTION: Retrocyclins - Antiviral and  
 ; TITLE OF INVENTION: Antimicrobial Peptides  
 ; FILE REFERENCE: UCLA-001CIP  
 ; CURRENT APPLICATION NUMBER: US/10/141,645 .  
 ; CURRENT FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: 60/284,855  
 ; PRIOR FILING DATE: 2001-04-18  
 ; PRIOR APPLICATION NUMBER: Unassigned  
 ; PRIOR FILING DATE: 2002-04-18  
 ; NUMBER OF SEQ ID NOS: 125

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 118  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: expansion of variant residues.  
US-10-141-645-118

Query Match 60.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 49  
US-10-141-645-119  
; Sequence 119, Application US/10141645  
; Publication No. US20030144184A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert Lehrer  
; APPLICANT: Alan Waring  
; APPLICANT: Alexander Cole  
; APPLICANT: Teresa Hong  
; TITLE OF INVENTION: Retrocyclins - Antiviral and  
; TITLE OF INVENTION: Antimicrobial Peptides  
; FILE REFERENCE: UCLA-001CIP  
; CURRENT APPLICATION NUMBER: US/10/141,645  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/284,855  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: Unassigned  
; PRIOR FILING DATE: 2002-04-18  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 119  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: expansion of variant residues.  
US-10-141-645-119

Query Match 60.0%; Score 3; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 50  
US-09-968-744A-234

```

; Sequence 234, Application US/09968744A
; Publication No. US20030148372A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073
; CURRENT APPLICATION NUMBER: US/09/968,744A
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-744A-234

```

```

Query Match          60.0%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      2 VLR 4
      |||
Db      4 VLR 6

```

```

Search completed: November 28, 2003, 15:43:19
Job time : 31 secs

```

OM protein - protein search, using sw model

Run on: November 28, 2003, 15:39:24 ; Search time 20 Seconds  
 (without alignments)  
 24.042 Million cell updates/sec

Title: US-09-228-866-46  
 Perfect score: 5  
 Sequence: 1 XVLRX 5

Scoring table: OLIGO  
 Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 7093

Minimum DB seq length: 5  
 Maximum DB seq length: 33

Post-processing: Listing first 100 summaries

Database : PIR\_76:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	%					Description
	Score	Query Match	Length	DB	ID	
1	3	60.0	14	2	S58426	spermadhesin AWN h
2	3	60.0	15	2	I49420	placental lactogen
3	3	60.0	17	2	PT0234	Ig heavy chain CRD
4	3	60.0	17	2	A60570	Ig mu heavy chain
5	3	60.0	19	2	A48354	nonstructural prot
6	3	60.0	19	2	S43641	carboxylesterase (
7	3	60.0	20	2	S18582	hypothetical prote
8	3	60.0	20	2	T50757	pufK protein [impo
9	3	60.0	20	2	PQ0046	citrate (si)-synth
10	3	60.0	20	2	PH1326	Ig heavy chain DJ
11	3	60.0	20	2	A13050	pyruvate kinase (E
12	3	60.0	20	4	I53672	somatotropin - syn
13	3	60.0	22	2	S19802	ubiquitin - potato



14	3	60.0	22	2	S03487	T-cell receptor be
15	3	60.0	23	2	S43469	heterodisulfide re
16	3	60.0	24	2	T42257	phosphoprotein pho
17	3	60.0	24	2	T42441	protein phosphatas
18	3	60.0	24	2	B43295	histone H4 - alfal
19	3	60.0	24	2	S53749	histone H4 - rat
20	3	60.0	24	2	B39433	ada 3'-region alkB
21	3	60.0	24	2	S32463	hydrogenase chain
22	3	60.0	25	2	PC4437	hydrogenase (EC 1.
23	3	60.0	25	2	PT0328	Ig heavy chain CDR
24	3	60.0	26	2	PQ0779	NADH2 dehydrogenas
25	3	60.0	26	2	I57726	major outer membra
26	3	60.0	27	2	JC1081	brain natriuretic
27	3	60.0	27	2	A81139	hypothetical prote
28	3	60.0	28	2	B47310	MHVS28AA - murine
29	3	60.0	29	2	S08088	gene VII protein -
30	3	60.0	29	2	A49288	alcohol dehydrogen
31	3	60.0	29	2	S35924	T-cell receptor ga
32	3	60.0	30	2	C95030	hypothetical prote
33	3	60.0	31	2	S13205	glyceraldehyde-3-p
34	3	60.0	31	2	S14727	glutathione transf
35	3	60.0	31	2	F82113	hypothetical prote
36	3	60.0	32	2	S35583	glutathione transf
37	3	60.0	32	2	PC4433	paired box transcr
38	3	60.0	32	2	S14300	zona pellucida-bin
39	3	60.0	33	2	B87660	hypothetical prote
40	2	40.0	5	2	S55237	zinc-binding prote
41	2	40.0	5	2	A60803	neuropeptide - sea
42	2	40.0	5	2	PT0278	Ig heavy chain CRD
43	2	40.0	6	2	A35890	RNA-directed DNA p
44	2	40.0	6	2	C22565	R-phycoerythrin be
45	2	40.0	6	2	A11490	pyruvate kinase (E
46	2	40.0	6	2	A49792	acylaminoacyl-pept
47	2	40.0	6	2	B33932	Ig mu chain D regi
48	2	40.0	6	2	I59142	platelet-derived g
49	2	40.0	6	2	PT0560	T-cell receptor be
50	2	40.0	7	2	ECMUCR	catch-relaxing pep
51	2	40.0	7	2	PQ0663	membrane protein -
52	2	40.0	7	2	S42407	gramicidin S synth
53	2	40.0	7	2	S70335	endosperm protein,
54	2	40.0	7	2	A28340	myomodulin - Calif
55	2	40.0	7	2	PT0246	Ig heavy chain CRD
56	2	40.0	7	2	E30608	Ig kappa chain V-I
57	2	40.0	7	2	PT0581	T-cell receptor be
58	2	40.0	7	2	S29735	polyphosphate-gluc
59	2	40.0	8	2	PH1407	Ig heavy chain V r
60	2	40.0	8	2	A39308	glycine reductase
61	2	40.0	8	2	PT0298	Ig heavy chain CRD
62	2	40.0	8	2	A42057	fibroblast growth
63	2	40.0	8	2	B47594	aspartate kinase (
64	2	40.0	9	2	D24180	fibrinogen beta ch
65	2	40.0	9	2	B60246	ornitho-kinin - ch
66	2	40.0	9	2	PS0253	glycine cleavage s
67	2	40.0	9	2	S13889	phosphoenolpyruvat
68	2	40.0	9	2	A60427	macrophage cytotox
69	2	40.0	9	2	S78426	52.5K protein - sp
70	2	40.0	9	4	I57650	hemoglobin alpha c

71	2	40.0	9	4	I73804	hypothetical E2 pr
72	2	40.0	10	1	RHPGG	gonadoliberin - pi
73	2	40.0	10	1	RHSHG	gonadoliberin - sh
74	2	40.0	10	2	A46491	C3 homolog HX - in
75	2	40.0	10	2	A60410	beta-neoendorphin
76	2	40.0	10	2	I36893	apolipoprotein A-I
77	2	40.0	10	2	B33710	ornithine decarbox
78	2	40.0	10	2	A32543	cardioexcitatory n
79	2	40.0	10	2	S39030	lysyl-bradykinin -
80	2	40.0	10	2	S13224	virG protein - Agr
81	2	40.0	10	2	S06964	hypothetical prote
82	2	40.0	10	2	S70722	65.4K GTP-binding
83	2	40.0	10	2	S42282	parasporal crystal
84	2	40.0	10	2	A44646	neurotoxin-associa
85	2	40.0	10	2	I44644	neurotoxin-associa
86	2	40.0	10	2	S66248	processing enzyme,
87	2	40.0	10	2	PS0451	24K protein 4302 -
88	2	40.0	10	2	A43977	FMRFamide-like pro
89	2	40.0	10	2	A56633	neomyosuppressin -
90	2	40.0	10	2	B45482	platelet activatin
91	2	40.0	10	2	A61354	carnitine medium/l
92	2	40.0	10	2	PC4374	telomeric and tetr
93	2	40.0	10	2	A61218	alpha-gliadin 4Ha
94	2	40.0	10	2	T17075	cytochrome-c oxida
95	2	40.0	10	2	PQ0788	NADH2 dehydrogenas
96	2	40.0	10	2	PQ0784	NADH2 dehydrogenas
97	2	40.0	11	2	A57458	gene Gax protein -
98	2	40.0	11	2	A55149	tetracenomycin A2
99	2	40.0	11	2	C59151	protein-tyrosine k
100	2	40.0	11	2	C61497	seed protein ws-18

## ALIGNMENTS

### RESULT 1

S58426

spermadhesin AWN homolog - horse (fragment)

C;Species: Equus caballus (domestic horse)

C;Date: 12-Feb-1998 #sequence\_revision 15-May-1998 #text\_change 07-May-1999

C;Accession: S58426

R;Calvete, J.J.; Mann, K.; Schaefer, W.; Sanz, L.; Reinert, M.; Nessau, S.; Raida, M.; Toepfer-Petersen, E.

Biochem. J. 310, 615-622, 1995

A;Title: Amino acid sequence of HSP-1, a major protein of stallion seminal plasma: effect of glycosylation on its heparin- and gelatin-binding capabilities.

A;Reference number: S58424; MUID:95382782; PMID:7654203

A;Accession: S58426

A;Molecule type: protein

A;Residues: 1-14 <CAL>

A;Experimental source: seminal plasma

Query Match 60.0%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            2 VLR 4  
             |||  
Db            12 VLR 14

RESULT 2

I49420

placental lactogen I - western wild mouse (fragment)

C;Species: Mus spretus (western wild mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000

C;Accession: I49420

R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.

Mamm. Genome 5, 349-355, 1994

A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A;Reference number: I48934; MUID:94319082; PMID:8043949

A;Accession: I49420

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-15 <RES>

A;Cross-references: EMBL:U05735; NID:g497071; PIDN:AAB60476.1; PID:g497072

C;Superfamily: prolactin

Query Match                    60.0%; Score 3; DB 2; Length 15;  
Best Local Similarity    100.0%; Pred. No. 6.3e+02;  
Matches        3; Conservative    0; Mismatches    0; Indels        0; Gaps        0;

Qy            2 VLR 4  
             |||  
Db            4 VLR 6

RESULT 3

PT0234

Ig heavy chain CRD3 region (clone 1-130) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0234

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0234

A;Molecule type: DNA

A;Residues: 1-17 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match                    60.0%; Score 3; DB 2; Length 17;  
Best Local Similarity    100.0%; Pred. No. 7e+02;  
Matches        3; Conservative    0; Mismatches    0; Indels        0; Gaps        0;

Qy            2 VLR 4  
             |||  
Db            6 VLR 8

RESULT 4

A60570

Ig mu heavy chain disease extra sequence - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 16-Aug-1996

C;Accession: A60570

R;Mihaesco, C.; Ferrara, P.; Guillemot, J.C.; Congy, N.; Gendron, M.C.; Roy, J.P.; Sizaret, P.Y.; Mihaesco, E.

Mol. Immunol. 27, 771-776, 1990

A;Title: A new extra sequence at the amino terminal of a mu heavy chain disease protein (DAG).

A;Reference number: A60570; MUID:90384486; PMID:2119480

A;Accession: A60570

A;Molecule type: protein

A;Residues: 1-17 <MIH>

C;Comment: This sequence is derived from the amino terminus of an abnormal immunoglobulin found in lymphoproliferative malignancies.

C;Keywords: immunoglobulin

Query Match 60.0%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 7e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 7 VLR 9

RESULT 5

A48354

nonstructural protein 4a - murine hepatitis virus (strain A59)

C;Species: murine hepatitis virus, MHV

C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 08-Oct-1999

C;Accession: A48354

R;Weiss, S.R.; Zoltick, P.W.; Leibowitz, J.L.

Arch. Virol. 129, 301-309, 1993

A;Title: The ns4 gene of mouse hepatitis virus (MHV), strain A 59 contains two ORFs and thus differs from ns4 of the JHM and S strains.

A;Reference number: A48354; MUID:93228453; PMID:8385918

A;Accession: A48354

A;Molecule type: genomic RNA

A;Residues: 1-19 <WEI>

A;Cross-references: GB:S58172; NID:g299093; PIDN:AAB26098.1; PID:g299094

A;Note: sequence extracted from NCBI backbone (NCBIN:129089, NCBIP:129090)

C;Keywords: nonstructural protein

Query Match 60.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

RESULT 6

S43641  
 carboxylesterase (EC 3.1.1.1), thermostable - Alicyclobacillus acidocaldarius  
 (fragment)  
 C;Species: Alicyclobacillus acidocaldarius  
 C;Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 17-Mar-1999  
 C;Accession: S43641  
 R;Manco, G.; di Gennaro, S.; de Rosa, M.; Rossi, M.  
 Eur. J. Biochem. 221, 965-972, 1994  
 A;Title: Purification and characterization of a thermostable carboxylesterase  
 from the thermoacidophilic eubacterium Bacillus acidocaldarius.  
 A;Reference number: S43641; MUID:94237161; PMID:8181479  
 A;Accession: S43641  
 A;Molecule type: protein  
 A;Residues: 1-19 <MAN>  
 A;Experimental source: strain MT3  
 A;Note: the source is designated as Bacillus acidocaldarius  
 C;Keywords: carboxylic ester hydrolase; monomer

Query Match 60.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 13 VLR 15

#### RESULT 7

S18582  
 hypothetical protein K (pufQ 3' region) - Rhodobacter sphaeroides  
 C;Species: Rhodobacter sphaeroides  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-May-1994  
 C;Accession: S18582; S32855  
 R;Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.  
 Mol. Microbiol. 5, 2649-2661, 1991  
 A;Title: DNA sequencing and complementation/deletion analysis of the bchA-puf  
 operon region of Rhodobacter sphaeroides: in vivo mapping of the oxygen-  
 regulated puf promoter.  
 A;Reference number: S18580; MUID:92140030; PMID:1779756  
 A;Accession: S18582  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-20 <HUN>  
 A;Cross-references: EMBL:X68795

Query Match 60.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 15 VLR 17

#### RESULT 8

T50757  
 pufK protein [imported] - Rhodobacter sphaeroides

C;Species: Rhodobacter sphaeroides  
C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000  
C;Accession: T50757  
R;Choudhary, M.; Kaplan, S.  
Nucleic Acids Res. 28, 862-867, 2000  
A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter  
sphaeroides 2.4.1.  
A;Reference number: Z25222; MUID:20115911; PMID:10648776  
A;Accession: T50757  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-20 <CHO>  
A;Cross-references: EMBL:AF195122; PIDN:AAF24301.1  
A;Experimental source: strain 2.4.1  
C;Genetics:  
A;Gene: pufK

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 15 VLR 17

#### RESULT 9

PQ0046

citrate (si)-synthase (EC 4.1.3.7) - Streptomyces hygroscopicus (fragment)  
N;Alternate names: citrate condensing enzyme; citrogenase; condensing enzyme;  
oxaloacetate transacetase  
C;Species: Streptomyces hygroscopicus  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 05-May-2000  
C;Accession: PQ0046  
R;Shimotohno, K.W.; Imai, S.; Murakami, T.; Seto, H.  
Agric. Biol. Chem. 54, 463-470, 1990  
A;Title: Purification and characterization of citrate synthase from Streptomyces  
hygroscopicus SF-1293 and comparison of its properties with those of 2-  
phosphinomethylmalic acid synthase.  
A;Reference number: PS0106; MUID:90334852; PMID:1368511  
A;Accession: PQ0046  
A;Molecule type: protein  
A;Residues: 1-20 <SHI>  
A;Experimental source: strain SF-1293  
C;Comment: This enzyme catalyzes the synthesis of citric acid.  
C;Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase; tricarboxylic acid  
cycle

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 6 VLR 8

RESULT 10

PH1326

Ig heavy chain DJ region (clone C515-116) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C;Accession: PH1326

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B  
precursor lymphoblastic leukemia as evidence for an in utero transforming event.

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1326

A;Molecule type: DNA

A;Residues: 1-20 <WAS>

C;Keywords: heterotetramer; immunoglobulin

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 1 VLR 3

RESULT 11

A13050

pyruvate kinase (EC 2.7.1.40) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 03-Mar-1995

C;Accession: A13050

R;Edlund, B.; Andersson, J.; Titanji, V.; Dahlqvist, U.; Ekman, P.; Zetterqvist,  
O.; Engstrom, L.

Biochem. Biophys. Res. Commun. 67, 1516-1521, 1975

A;Title: Amino acid sequence at the phosphorylated site of rat liver pyruvate  
kinase.

A;Reference number: A13050; MUID:76088052; PMID:1106423

A;Accession: A13050

A;Molecule type: protein

A;Residues: 1-20 <EDL>

A;Experimental source: liver

C;Keywords: glycolysis; phosphotransferase

Query Match 60.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 8e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 11 VLR 13

RESULT 12

I53672

somatotropin - synthetic

C;Species: synthetic

C;Date: 07-Jun-1996 #sequence\_revision 31-Jul-1997 #text\_change 19-May-2000

C;Accession: I53672  
 R;Bogosian, G.; Bilyeu, K.; O'Neil, J.P.  
 Gene 133, 17-22, 1993  
 A;Title: Genome rearrangements by residual IS10 elements in strains of Escherichia coli K-12 which had undergone Tn10 mutagenesis and fusaric acid selection.  
 A;Reference number: I53672; MUID:94040791; PMID:8224890  
 A;Accession: I53672  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-20 <BOG>  
 A;Cross-references: GB:S67119; NID:g455674; PIDN:AAB28847.1; PID:g455675  
 A;Note: partial sequence of bovine somatotropin synthesized and expressed in Escherichia coli fusion protein

Query Match 60.0%; Score 3; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 8e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 15 VLR 17

#### RESULT 13

S19802  
 ubiquitin - potato (fragment)  
 C;Species: Solanum tuberosum (potato)  
 C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Jul-2000  
 C;Accession: T07823; S19802  
 R;Garbarino, J.E.; Rockhold, D.R.; Belknap, W.R.  
 Plant Mol. Biol. 20, 235-244, 1992  
 A;Title: Expression of stress-responsive ubiquitin genes in potato tubers.  
 A;Reference number: S25305; MUID:93004476; PMID:1327270  
 A;Accession: T07823  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-22 <GAR>  
 A;Cross-references: EMBL:Z11668; NID:g21609; PIDN:CAA77734.2; PID:g4468034  
 A;Experimental source: cv. Lemhi Russet; tuber disc  
 C;Superfamily: ubiquitin; ubiquitin homology

Query Match 60.0%; Score 3; DB 2; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 14 VLR 16

#### RESULT 14

S03487  
 T-cell receptor beta chain J region (clone HBP22) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 30-May-1997  
 C;Accession: S03487



R;Kimura, N.; Toyonaga, B.; Yoshikai, Y.; Triebel, F.; Debre, P.; Minden, M.D.; Mak, T.W.

J. Exp. Med. 164, 739-750, 1986

A;Title: Sequences and diversity of human T cell receptor beta chain variable region genes.

A;Reference number: S03485; MUID:86306525; PMID:3755748

A;Accession: S03487

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-22 <KIM>

A;Cross-references: EMBL:X04923

C;Keywords: T-cell receptor

Query Match 60.0%; Score 3; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 6 VLR 8

#### RESULT 15

S43469

heterodisulfide reductase (EC 1.12.99.-) small chain - Methanosarcina barkeri (fragment)

C;Species: Methanosarcina barkeri

C;Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 01-Feb-1999

C;Accession: S43469

R;Heiden, S.; Hedderich, R.; Setzke, E.; Thauer, R.K.

Eur. J. Biochem. 221, 855-861, 1994

A;Title: Purification of a two-subunit cytochrome-b-containing heterodisulfide reductase from methanol-grown Methanosarcina barkeri.

A;Reference number: S43468; MUID:94229084; PMID:8174566

A;Accession: S43469

A;Molecule type: protein

A;Residues: 1-23 <HEI>

A;Experimental source: strain Fusaro

C;Genetics:

A;Gene: hdrE

C;Complex: heterodimer; large chain and small chain

C;Function:

A;Description: catalyzes the reduction of the heterodisulfide of coenzyme M and 7-mercaptoheptanoyl-L-threonine phosphate with molecular hydrogen, which is coupled with electronic proton translocation

A;Pathway: energy-conserving electron-transport chain

A;Note: terminal step in pathway

C;Keywords: heterodimer; oxidoreductase; electron transfer; heme

Query Match 60.0%; Score 3; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 13 VLR 15

# RESULT 16

T42257

phosphoprotein phosphatase (EC 3.1.3.16) - *Caenorhabditis elegans* (fragment)

C;Species: *Caenorhabditis elegans*

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 02-Jun-2000

C;Accession: T42257

R;Zeke, T.; Gergely, P.; Dombradi, V.

submitted to the EMBL Data Library, July 1996

A;Description: The catalytic subunits of Ser/Thr protein phosphatases from *Caenorhabditis elegans*: a biochemical and molecular biological survey.

A;Reference number: Z22131

A;Accession: T42257

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-24 <ZEK>

A;Cross-references: EMBL:Z77735; PIDN:CAB01294.1

C;Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein phosphatase homology

C;Keywords: phosphoric monoester hydrolase

Query Match 60.0%; Score 3; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

# RESULT 17

T42441

protein phosphatase - *Caenorhabditis elegans* (fragment)

C;Species: *Caenorhabditis elegans*

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 02-Jun-2000

C;Accession: T42441

R;Zeke, T.; Gergely, P.; Dombradi, V.

submitted to the EMBL Data Library, July 1996

A;Description: The catalytic subunits of Ser/Thr protein phosphatases from *Caenorhabditis elegans*: a biochemical and molecular biological survey.

A;Reference number: Z22131

A;Accession: T42441

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-24 <ZEK>

A;Cross-references: EMBL:Z77729; PIDN:CAB01288.1

C;Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein phosphatase homology

Query Match 60.0%; Score 3; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 5 VLR 7

# RESULT 18

B43295

histone H4 - alfalfa (fragment)

C;Species: Medicago sativa (alfalfa)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 12-Apr-1995

C;Accession: B43295

R;Waterborg, J.H.

Biochemistry 31, 6211-6219, 1992

A;Title: Identification of five sites of acetylation in alfalfa histone H4.

A;Reference number: A43295; MUID:92329443; PMID:1627562

A;Accession: B43295

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-24 <WAT>

C;Superfamily: histone H4

Query Match 60.0%; Score 3; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 9.3e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4

|||

Db 21 VLR 23

# RESULT 19

S53749

histone H4 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 03-May-1996

C;Accession: S53749

R;Baneres, J.L.; Essalouh, L.; Jariel-Encontre, I.; Mesnier, D.; Garrod, S.; Parello, J.

J. Mol. Biol. 243, 48-59, 1994

A;Title: Evidence indicating proximity in the nucleosome between the histone H4 N termini and the globular domain of histone H1.

A;Reference number: S53749; MUID:95018250; PMID:7932740

A;Accession: S53749

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-24 <BAN>

C;Superfamily: histone H4

Query Match 60.0%; Score 3; DB 2; Length 24;

Best Local Similarity 100.0%; Pred. No. 9.3e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4

|||

Db 14 VLR 16

# RESULT 20

B39433

ada 3'-region alkB homolog - Salmonella typhimurium (fragment)

C;Species: Salmonella typhimurium

C;Date: 21-Feb-1992 #sequence\_revision 21-Feb-1992 #text\_change 30-Sep-1993  
C;Accession: B39433  
R;Hakura, A.; Morimoto, K.; Sofuni, T.; Nohmi, T.  
J. Bacteriol. 173, 3663-3672, 1991  
A;Title: Cloning and characterization of the Salmonella typhimurium ada gene,  
which encodes O(6)-methylguanine-DNA methyltransferase.  
A;Reference number: A39433; MUID:91267928; PMID:1904855  
A;Accession: B39433  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-24 <HAK>  
A;Cross-references: GB:D90221  
C;Superfamily: alkB protein

Query Match 60.0%; Score 3; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 21 VLR 23

#### RESULT 21

S32463

hydrogenase chain vhuU - Methanococcus voltae

C;Species: Methanococcus voltae

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997

C;Accession: S32463

R;Sorgenfrei, O.; Linder, D.; Karas, M.; Klein, A.

Eur. J. Biochem. 213, 1355-1358, 1993

A;Title: A novel very small subunit of a selenium containing [NiFe] hydrogenase  
of Methanococcus voltae is postranslationally processed by cleavage at a defined  
position.

A;Reference number: S32463; MUID:93279338; PMID:8504827

A;Accession: S32463

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-24 <SOR>

Query Match 60.0%; Score 3; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 13 VLR 15

#### RESULT 22

PC4437

hydrogenase (EC 1.18.99.1) (NiFe) - Desulfovibrio vulgaris (fragment)

C;Species: Desulfovibrio vulgaris

C;Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 07-May-1999

C;Accession: PC4437

R;Romas, C.V.; Pereira, I.A.C.; Xavier, A.V.; LeGall, J.; Teixeira, M.

Biochem. Biophys. Res. Commun. 240, 75-79, 1997

A;Title: Characterization of the [NiFe] hydrogenase from the sulfate reducer  
Desulfovibrio vulgaris hildenborough.

A;Reference number: PC4437; MUID:98042519; PMID:9367885

A;Accession: PC4437

A;Molecule type: protein

A;Residues: 1-25 <ROM>

C;Keywords: oxidoreductase

Query Match 60.0%; Score 3; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 21 VLR 23

#### RESULT 23

PT0328

Ig heavy chain CDR3 region (clone J2-118) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 02-Feb-2001

C;Accession: PT0328

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain  
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0328

A;Molecule type: DNA

A;Residues: 1-25 <YAM>

A;Experimental source: B lymphocyte

A;Note: the authors translated the stop codon for residue 14 as X

C;Keywords: heterotetramer; immunoglobulin

Query Match 60.0%; Score 3; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 16 VLR 18

#### RESULT 24

PQ0779

NADH2 dehydrogenase (EC 1.6.99.3) 42K chain - fava bean mitochondrion (fragment)

N;Alternate names: complex I 42K chain; NADH-ubiquinone reductase 42K chain

C;Species: mitochondrion Vicia faba (fava bean)

C;Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 03-Jun-2002

C;Accession: PQ0779

R;Leterme, S.; Boutry, M.

Plant Physiol. 102, 435-443, 1993

A;Title: Purification and preliminary characterization of mitochondrial complex  
I (NADH:ubiquinone reductase) from broad bean (Vicia faba L.).

A;Reference number: PQ0775; MUID:94151437; PMID:8108509

A;Accession: PQ0779

A;Molecule type: protein  
A;Residues: 1-26 <LET>  
C;Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the three proton-translocating complexes of the mitochondrial respiratory chain and composed of 35 different subunits ranging from 5K to 75K.  
C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by a large number of redox groups.  
C;Genetics:  
A;Genome: mitochondrion  
C;Superfamily: NADH dehydrogenase (ubiquinone) 49K protein  
C;Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 60.0%; Score 3; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 24 VLR 26

#### RESULT 25

I57726

major outer membrane protein A(3b) - Escherichia coli

C;Species: Escherichia coli

C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 08-Oct-1999

C;Accession: I57726

R;Gordon, G.; Gayda, R.C.; Markovitz, A.

Mol. Gen. Genet. 193, 414-421, 1984

A;Title: Sequence of the regulatory region of omp T, the gene specifying major outer membrane protein a (3b) of Escherichia coli K-12: implications for regulation and processing.

A;Reference number: I57726; MUID:84167352; PMID:6323918

A;Accession: I57726

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-26 <RES>

A;Cross-references: EMBL:X00348; NID:g42163; PIDN:CAA25097.1; PID:g42164

Query Match 60.0%; Score 3; DB 2; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 15 VLR 17

#### RESULT 26

JC1081

brain natriuretic peptide - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 27-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 16-Feb-1997

C;Accession: JC1081

R;Chen, H.; Zhang, J.; Wang, Q.S.; Cui, H.; Tang, J.

J. Fudan Univ. (Natur. Sci.) 30, 413-416, 1991

A;Title: Chemical synthesis and cloning of the porcine brain natriuretic gene.

A;Reference number: JC1081  
A;Accession: JC1081  
A;Molecule type: DNA  
A;Residues: 1-27 <CHE>  
A;Note: The translation of the start codon ATG is not given in this paper  
C;Genetics:  
A;Gene: bnp  
C;Superfamily: natriuretic peptide A precursor  
C;Keywords: brain; natriuretic

Query Match 60.0%; Score 3; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 23 VLR 25

#### RESULT 27

A81139

hypothetical protein NMB0953 [imported] - Neisseria meningitidis (strain MC58 serogroup B)

C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

C;Accession: A81139

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Ketchum, K.A.; Hood, D.W.; Peden, J.F.; Dodson, R.J.; Nelson, W.C.; Gwinn, M.L.; DeBoy, R.; Peterson, J.D.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Mason, T.; Ciecko, A.; Parksey, D.S.; Blair, E.; Cittone, H.; Clark, E.B.; Cotton, M.D.; Utterback, T.R.; Khouri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Venter, J.C.

A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Accession: A81139

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-27 <TET>

A;Cross-references: GB:AE002446; GB:AE002098; NID:g7226185; PIDN:AAF41359.1; PID:g7226192; GSPDB:GN00119; TIGR:NMB0953

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NMB0953

Query Match 60.0%; Score 3; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 23 VLR 25

RESULT 28

B47310

MHVS28AA - murine hepatitis virus

C;Species: murine hepatitis virus, MHV

C;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999

C;Accession: B47310

R;Schaad, M.C.; Baric, R.S.

Virology 196, 190-198, 1993

A;Title: Evidence for new transcriptional units encoded at the 3' end of the mouse hepatitis virus genome.

A;Reference number: A47310; MUID:93362405; PMID:8395114

A;Contents: A59

A;Accession: B47310

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-28 <SCH>

A;Cross-references: GB:S64884; NID:g408334; PIDN:AAB27903.1; PID:g408336

A;Note: sequence extracted from NCBI backbone (NCBIN:136580, NCBIP:136582)

Query Match 60.0%; Score 3; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 24 VLR 26

RESULT 29

S08088

gene VII protein - phage I2-2

C;Species: phage I2-2

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Sep-1999

C;Accession: S08088

R;Schoenmakers, H.F.P.M.; Yu, M.; Konings, R.N.H.

submitted to the EMBL Data Library, February 1989

A;Reference number: S08084

A;Accession: S08088

A;Molecule type: DNA

A;Residues: 1-29 <SCH>

A;Cross-references: EMBL:X14336; NID:g14920; PIDN:CAA32515.1; PID:g14926

C;Genetics:

A;Gene: VII

C;Superfamily: class I filamentous phage coat protein C chain I

Query Match 60.0%; Score 3; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 27 VLR 29

RESULT 30

A49288



alcohol dehydrogenase (acceptor) (EC 1.1.99.8) - Acetobacter methanolicus (fragment)  
 N;Alternate names: type II methanol dehydrogenase  
 C;Species: Acetobacter methanolicus  
 C;Date: 24-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Oct-1998  
 C;Accession: A49288  
 R;Matsushita, K.; Takahashi, K.; Adachi, O.  
 Biochemistry 32, 5576-5582, 1993  
 A;Title: A novel quinoprotein methanol dehydrogenase containing an additional 32-kilodalton peptide purified from Acetobacter methanolicus: identification of the peptide as a MoxJ product.  
 A;Reference number: A49288; MUID:93277836; PMID:8389187  
 A;Accession: A49288  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-29 <MAT>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:133048)  
 C;Keywords: alcohol metabolism; oxidoreductase

Query Match 60.0%; Score 3; DB 2; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 6 VLR 8

#### RESULT 31

S35924

T-cell receptor gamma chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 30-Jun-2001

C;Accession: S35924

R;Mathioudakis, G.; Platsoucas, C.D.

submitted to the EMBL Data Library, May 1993

A;Description: An alternative splicing between V-gamma, J-gamma2.3 and C-gamma2 gene segments of the gamma-chain T-cell receptor transcripts from peripheral blood lymphocytes from normal donors.

A;Reference number: S32764

A;Accession: S35924

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-29 <MAT>

A;Cross-references: EMBL:Z22684

C;Keywords: T-cell receptor

Query Match 60.0%; Score 3; DB 2; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 1 VLR 3

#### RESULT 32

C95030

hypothetical protein SP0258 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001

C;Accession: C95030

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: C95030

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-30 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74436.1; PID:gl4971728; GSPDB:GN00164; TIGR:SP4SP0258

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0258

Query Match 60.0%; Score 3; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4

|||

Db 18 VLR 20

RESULT 33

S13205

glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) I - fungus (Trichoderma koningii) (fragment)

C;Species: Trichoderma koningii

C;Date: 21-Nov-1993 #sequence\_revision 21-Jul-1995 #text\_change 03-Jun-2002

C;Accession: S13205

R;Sakai, K.; Hasumi, K.; Endo, A.

Eur. J. Biochem. 193, 195-202, 1990

A;Title: Two glyceraldehyde-3-phosphate dehydrogenase isozymes from the koningic acid (heptelidic acid) producer Trichoderma koningii.

A;Reference number: S13205; MUID:91031446; PMID:2226438

A;Accession: S13205

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-31 <EUR>

A;Experimental source: strain M3947

C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase

C;Keywords: gluconeogenesis; glycolysis; homotetramer; NAD; oxidoreductase

Query Match 60.0%; Score 3; DB 2; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
|||  
Db 16 VLR 18

RESULT 34

S14727

glutathione transferase (EC 2.5.1.18) 7.3 - *Serratia marcescens* (fragment)

C;Species: *Serratia marcescens*

C;Date: 19-Mar-1997 #sequence\_revision 30-Jan-1998 #text\_change 01-Feb-1999

C;Accession: S14727

R;di Ilio, C.; Aceto, A.; Piccolomini, R.; Allocati, N.; Faraone, A.;

Bucciarelli, T.; Barra, D.; Federici, G.

Biochim. Biophys. Acta 1077, 141-146, 1991

A;Title: Purification and characterization of a novel glutathione transferase from *Serratia marcescens*.

A;Reference number: S14727; MUID:91198121; PMID:2015287

A;Accession: S14727

A;Molecule type: protein

A;Residues: 1-31 <ILL>

A;Experimental source: strain CIP 6755

C;Complex: homodimer

C;Function:

A;Description: catalyzes conjugation of glutathione to a large variety of electrophilic compounds of endobiotic and xenobiotic origin; also involved in intracellular binding and transport of hydrophobic compounds; involved in detoxification of organic hydroperoxides

C;Superfamily: glutathione transferase

C;Keywords: homodimer; transferase

Query Match 60.0%; Score 3; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
|||  
Db 17 VLR 19

RESULT 35

F82113

hypothetical protein VC2155 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C;Accession: F82113

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.;

Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill,

S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.;

Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.;

Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.;

Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: F82113  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-31 <HEI>  
A;Cross-references: GB:AE004287; GB:AE003852; NID:g9656689; PIDN:AAF95300.1; GSPDB:GN00126; TIGR:VC2155  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC2155  
A;Map position: 1

Query Match 60.0%; Score 3; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 22 VLR 24

RESULT 36

S35583

glutathione transferase (EC 2.5.1.18) - *Xanthomonas campestris* (fragment)

C;Species: *Xanthomonas campestris*

C;Date: 19-Mar-1997 #sequence\_revision 30-Jan-1998 #text\_change 17-Mar-1999

C;Accession: S35583

R;di Ilio, C.; Aceto, A.; Allocati, N.; Piccolomini, R.; Bucciarelli, T.;

Dragani, B.; Faraone, A.; Sacchetta, P.; Petruzzelli, R.; Federici, G.

Arch. Biochem. Biophys. 305, 110-114, 1993

A;Title: Characterization of glutathione transferase from *Xanthomonas campestris*.

A;Reference number: S35583; MUID:93343617; PMID:8342943

A;Accession: S35583

A;Molecule type: protein

A;Residues: 1-32 <ILI>

C;Complex: dimer

C;Function:

A;Description: catalyzes conjugation of glutathione to a large variety of electrophilic compounds of endobiotic and xenobiotic origin; also involved in intracellular binding and transport of hydrophobic compounds; involved in detoxification of organic hydroperoxides

C;Superfamily: glutathione transferase

C;Keywords: dimer; transferase

Query Match 60.0%; Score 3; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 17 VLR 19

RESULT 37

PC4433

paired box transcription factor Pax-6 splice form 3 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 15-Oct-1999

C;Accession: PC4433

R;Jaworski, C.; Sperbeck, S.; Graham, C.; Wistow, G.

Biochem. Biophys. Res. Commun. 240, 196-202, 1997

A;Title: Alternative splicing of Pax6 in bovine eye and evolutionary conservation of intron sequences.

A;Reference number: PC4431; MUID:98042543; PMID:9367909

A;Accession: PC4433

A;Molecule type: mRNA

A;Residues: 1-32 <JAW>

A;Cross-references: GB:U73855

C;Comment: This protein is involved in eye development and in tissue specific gene expression within the eye.

C;Superfamily: paired box transcription factor Pax-6; homeobox homology; paired box homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 60.0%; Score 3; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 30 VLR 32

RESULT 38

S14300

zona pellucida-binding glycoprotein - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 13-Sep-1998

C;Accession: S14300

R;Jonakova, V.; Sanz, L.; Calvete, J.J.; Henschen, A.; Cechova, D.; Toepfer-Petersen, E.

FEBS Lett. 280, 183-186, 1991

A;Title: Isolation and biochemical characterization of a zona pellucida-binding glycoprotein of boar spermatozoa.

A;Reference number: S14300; MUID:91184410; PMID:1849093

A;Accession: S14300

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-32 <JON>

C;Superfamily: spermadhesin

Query Match 60.0%; Score 3; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 12 VLR 14

RESULT 39

B87660

hypothetical protein CC3316 [imported] - *Caulobacter crescentus*

C;Species: *Caulobacter crescentus*

C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C;Accession: B87660

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.; Alley, M.; Ohta, N.; Maddock, J.R.; Potocka, I.; Nelson, W.C.; Newton, A.; Stephens, C.; Phadke, N.D.; Ely, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonay, J.F.; Smit, J.; Craven, M.; Khouri, H.; Shetty, J.; Berry, K.; Utterback, T.; Tran, K.; Wolf, A.; Vamathevan, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of *Caulobacter crescentus*.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: B87660

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-33 <STO>

A;Cross-references: GB:AE005673; NID:g13425012; PIDN:AAK25278.1; GSPDB:GN00148

C;Genetics:

A;Gene: CC3316

Query Match 60.0%; Score 3; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 29 VLR 31

#### RESULT 40

S55237

zinc-binding protein ZBP14 - maize (fragment)

C;Species: *Zea mays* (maize)

C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 07-May-1999

C;Accession: S55237

R;Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A. Biochem. J. 307, 267-272, 1995

A;Title: Expression and characterization of maize ZBP14, a member of a new family of zinc-binding proteins.

A;Reference number: S55237; MUID:95234046; PMID:7717986

A;Accession: S55237

A;Molecule type: protein

A;Residues: 1-5 <ROB>

Query Match 40.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
||  
Db 4 VL 5

#### RESULT 41

A60803  
 neuropeptide - sea anemone (*Anthopleura elegantissima*)  
 C;Species: *Anthopleura elegantissima*  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: A60803  
 R;Graff, D.; Grimmelikhuijzen, C.J.P.  
 Brain Res. 442, 354-358, 1988  
 A;Title: Isolation of <Glu-Ser-Lu-Arg-Trp-NH-2, a novel neuropeptide from sea anemones.  
 A;Reference number: A60803; MUID:88222764; PMID:2897223  
 A;Accession: A60803  
 A;Molecule type: protein  
 A;Residues: 1-5 <GRA>  
 C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F;5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 3 LR 4

#### RESULT 42

PT0278  
 Ig heavy chain CRD3 region (clone 4-88) - human (fragment)  
 C;Species: *Homo sapiens* (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C;Accession: PT0278  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in adult human peripheral blood B lymphocytes.  
 A;Reference number: PT0222; MUID:91108337; PMID:1899102  
 A;Accession: PT0278  
 A;Molecule type: DNA  
 A;Residues: 1-5 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
 ||  
 Db 4 VL 5

#### RESULT 43

A35890  
 RNA-directed DNA polymerase (EC 2.7.7.49) 66K chain - human immunodeficiency virus type 1 (fragment)  
 C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 31-Dec-1993  
C;Accession: A35890  
R;Bathurst, I.C.; Moen, L.K.; Lujan, M.A.; Gibson, H.L.; Feucht, P.H.;  
Pichuantes, S.; Craik, C.S.; Santi, D.V.; Barr, P.J.  
Biochem. Biophys. Res. Commun. 171, 589-595, 1990  
A;Title: Characterization of the human immunodeficiency virus type-1 reverse  
transcriptase enzyme produced in yeast.  
A;Reference number: A35890; MUID:90386627; PMID:1698361  
A;Accession: A35890  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <BAT>  
C;Keywords: nucleotidyltransferase

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
||  
Db 5 VL 6

#### RESULT 44

C22565

R-phycoerythrin beta-1 chain - red alga (*Gastroclonium coulteri*) (fragment)

C;Species: *Gastroclonium coulteri*

C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993

C;Accession: C22565

R;Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A;Reference number: A22565; MUID:85182601; PMID:3886644

A;Accession: C22565

A;Molecule type: protein

A;Residues: 1-6 <KLO>

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 5 LR 6

#### RESULT 45

A11490

pyruvate kinase (EC 2.7.1.40) - pig (fragment)

C;Species: *Sus scrofa domestica* (domestic pig)

C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 03-Mar-1995

C;Accession: A11490

R;Hjelmquist, G.; Andersson, J.; Edlund, B.; Engstrom, L.

Biochem. Biophys. Res. Commun. 61, 559-563, 1974

A;Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate  
kinase phosphorylated by cyclic 3',5'-AMP-stimulated protein kinase and gamma-  
(32-P)ATP.



A;Reference number: A11490; MUID:75127438; PMID:4375989

A;Accession: A11490

A;Molecule type: protein

A;Residues: 1-6 <HJE>

A;Experimental source: liver

C;Keywords: glycolysis; phosphotransferase

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4

||

Db 1 LR 2

#### RESULT 46

A49792

acylaminoacyl-peptidase (EC 3.4.19.1) - rabbit (fragment)

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999

C;Accession: A49792

R;Krishna, R.G.; Chin, C.C.Q.; Wold, F.

Anal. Biochem. 199, 45-50, 1991

A;Title: N-terminal sequence analysis of N(alpha)-acetylated proteins after unblocking with N-acylaminoacyl-peptide hydrolase.

A;Reference number: A49792; MUID:92222120; PMID:1807161

A;Accession: A49792

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-6 <KRI>

C;Keywords: acetylated amino end; hydrolase; omega peptidase

F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3

||

Db 5 VL 6

#### RESULT 47

B33932

Ig mu chain D region (D23) - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 16-Aug-1996

C;Accession: B33932

R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.

Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989

A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-line genes.

A;Reference number: A33932; MUID:89282823; PMID:2499887

A;Accession: B33932

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-6 <BAC>  
A;Cross-references: GB:M27107  
C;Keywords: immunoglobulin

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 3 LR 4

RESULT 48

I59142

platelet-derived growth factor B chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C;Accession: I59142

R;Pech, M.; Gazit, A.; Arnstein, P.; Aaronson, S.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 2693-2697, 1989

A;Title: Generation of fibrosarcomas in vivo by a retrovirus that expressed the normal B chain of platelet-derived growth factor and mimics the alternative splice pattern of the v-sis oncogene.

A;Reference number: I59142; MUID:89202393; PMID:2649890

A;Accession: I59142

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-6 <RES>

A;Cross-references: GB:M26180; NID:g516624; PIDN:AAA39905.1; PID:g516625

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
||  
Db 5 VL 6

RESULT 49

PT0560

T-cell receptor beta chain V-D-J region (126-1CE) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0560

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0560

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 40.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
||  
Db 3 VL 4

RESULT 50

ECMUCR

catch-relaxing peptide - blue mussel

N;Alternate names: CARP

C;Species: Mytilus edulis (blue mussel)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000

C;Accession: A29342

R;Hirata, T.; Kubota, I.; Takabatake, I.; Kawahara, A.; Shimamoto, N.; Muneoka, Y.

Brain Res. 422, 374-376, 1987

A;Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.

A;Reference number: A29342; MUID:88052022; PMID:3676797

A;Accession: A29342

A;Molecule type: protein

A;Residues: 1-7 <HIR>

C;Comment: This peptide exhibits both potentiating (contraction) and inhibitory (relaxation) effects on the anterior byssus retractor muscle.

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; hormone; retractor muscle

F;7/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 40.0%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 5 LR 6

Search completed: November 28, 2003, 15:42:04

Job time : 22 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 15:39:24 ; Search time 10 Seconds  
(without alignments)  
23.513 Million cell updates/sec

Title: US-09-228-866-46  
Perfect score: 5  
Sequence: 1 XVLRX 5

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2296

Minimum DB seq length: 5  
Maximum DB seq length: 33

Post-processing: Listing first 100 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3	60.0	20	1	CISY_STRHY	P20903	streptomyce
2	3	60.0	20	1	OMPW_VIBAL	P83151	vibrio algi
3	3	60.0	20	1	PUFK_RHOSH	Q53121	rhodobacter
4	3	60.0	26	1	RL36_DESDE	Q46501	desulfovibr
5	3	60.0	27	1	L52_ADE07	P05663	human adeno
6	3	60.0	29	1	COA1_BPI22	P15413	bacteriopha
7	3	60.0	31	1	GT_SERMA	P22416	serratia ma
8	3	60.0	31	1	PETL_MESVI	Q9mun4	mesostigma
9	2	40.0	6	1	ACPH_RABIT	P25154	oryctolagus
10	2	40.0	7	1	CARP_MYTED	P10420	mytilus edu
11	2	40.0	7	1	FAR1_HELTI	P41871	helisoma tr
12	2	40.0	7	1	FAR1_MACRS	P83274	macrobrachi
13	2	40.0	7	1	FAR1_PROCL	P38499	procambarus
14	2	40.0	7	1	FAR2_ASCSU	P31890	ascaris suu
15	2	40.0	7	1	FAR2_PROCL	P38498	procambarus
16	2	40.0	8	1	CAD1_ENTFA	P13268	enterococcu
17	2	40.0	8	1	COW2_CONPU	P58785	conus purpu

18	2	40.0	8	1	FAR1_PANRE	P41872	panagrellus
19	2	40.0	8	1	FAR1_PENMO	P83316	penaeus mon
20	2	40.0	8	1	FAR2_MACRS	P83275	macrobrachi
21	2	40.0	8	1	FAR3_HOMAM	P41486	homarus ame
22	2	40.0	8	1	FAR4_HOMAM	P41487	homarus ame
23	2	40.0	8	1	FAR4_MACRS	P83277	macrobrachi
24	2	40.0	9	1	BS43_SERPL	P83375	serratia pl
25	2	40.0	9	1	FAR2_PANRE	P41873	panagrellus
26	2	40.0	9	1	FAR3_MACRS	P83276	macrobrachi
27	2	40.0	9	1	FAR3_PENMO	P83318	penaeus mon
28	2	40.0	9	1	FAR4_PENMO	P83319	penaeus mon
29	2	40.0	9	1	FAR5_PENMO	P83320	penaeus mon
30	2	40.0	9	1	FAR6_MACRS	P83279	macrobrachi
31	2	40.0	9	1	FAR8_MACRS	P83281	macrobrachi
32	2	40.0	9	1	FAR9_ASCSU	P43172	ascaris suu
33	2	40.0	9	1	FARP_CALSI	P38495	callinectes
34	2	40.0	9	1	FIBB_ERYPA	P19346	erythrocebu
35	2	40.0	10	1	BRK_ONCMY	Q9prz1	oncorhynchu
36	2	40.0	10	1	ESL_LACCA	P81758	lactobacill
37	2	40.0	10	1	FAR2_PENMO	P83317	penaeus mon
38	2	40.0	10	1	FAR5_MACRS	P83278	macrobrachi
39	2	40.0	10	1	FAR7_MACRS	P83280	macrobrachi
40	2	40.0	10	1	FARP_LOCFI	P38553	locusta mig
41	2	40.0	10	1	FARP_MANSE	P18523	manduca sex
42	2	40.0	10	1	LCMS_LEUMA	P21144	leucophaea
43	2	40.0	10	1	PORB_METTM	P80901	methanobact
44	2	40.0	10	1	TKU1_UREUN	P40751	urechis uni
45	2	40.0	10	1	UPA5_HUMAN	P30091	homo sapien
46	2	40.0	11	1	ES1_RAT	P56571	rattus norv
47	2	40.0	11	1	FAR6_PENMO	P83321	penaeus mon
48	2	40.0	12	1	RR16_GINBI	P36207	ginkgo bilo
49	2	40.0	12	1	TM2A_METMA	P80652	methanosarc
50	2	40.0	13	1	CRBL_VESCR	P01518	vespa crabr
51	2	40.0	13	1	FARB_ASCSU	P43173	ascaris suu
52	2	40.0	13	1	FIBB_RABIT	P14478	oryctolagus
53	2	40.0	13	1	PEDI_HYDAT	P80578	hydra atten
54	2	40.0	13	1	SA2A_ONCMY	P82238	oncorhynchu
55	2	40.0	13	1	SA2B_ONCMY	P82239	oncorhynchu
56	2	40.0	13	1	TEMA_RANTE	P56917	rana tempor
57	2	40.0	13	1	TEME_RANTE	P56920	rana tempor
58	2	40.0	13	1	TEMF_RANTE	P56921	rana tempor
59	2	40.0	13	1	UN12_CLOPA	P81353	clostridium
60	2	40.0	13	1	YPNP_PHOLU	P41122	photorhabdu
61	2	40.0	14	1	BGAT_MOUSE	P38649	m histo-blo
62	2	40.0	14	1	KLPS_SCARA	P58396	scaptocosa
63	2	40.0	14	1	LPER_BACLI	Q04303	bacillus li
64	2	40.0	14	1	LPW_CITFR	P03056	citrobacter
65	2	40.0	14	1	LPW_ECOLI	P03053	escherichia
66	2	40.0	14	1	MAST_POLJA	P01517	polistes ja
67	2	40.0	14	1	MAST_VESBA	P21654	vespa basal
68	2	40.0	14	1	MAST_VESOR	P17238	vespa orien
69	2	40.0	14	1	NEJ2_FASHE	P80526	fasciola he
70	2	40.0	15	1	ACT_PINPS	P81085	pinus pinas
71	2	40.0	15	1	AF1L_MALPA	P83141	malva parvi
72	2	40.0	15	1	ATP2_PINPS	P81663	pinus pinas
73	2	40.0	15	1	CDN4_LITCE	P82076	litoria cae
74	2	40.0	15	1	GTS_ASADI	P83246	asaphis dic

75	2	40.0	15	1	IRBP_CRISP	P12665 cricetidae
76	2	40.0	15	1	KLOM_LUMTE	P11918 lumbricus t
77	2	40.0	15	1	LPL_THETH	P21234 thermus the
78	2	40.0	15	1	PH3_PRUSE	P29265 prunus sero
79	2	40.0	15	1	RKGG_CARCR	P21586 caretta car
80	2	40.0	15	1	UC27_MAIZE	P80633 zea mays (m
81	2	40.0	15	1	UC28_MAIZE	P80634 zea mays (m
82	2	40.0	15	1	YAA3_RHOPA	Q02006 rhodopseudo
83	2	40.0	16	1	ALRX_PSEPU	P17916 pseudomonas
84	2	40.0	16	1	BRB_BASAL	P83187 basella alb
85	2	40.0	16	1	CFAB_BOVIN	P81187 bos taurus
86	2	40.0	16	1	H5_COTJA	P18638 coturnix co
87	2	40.0	16	1	HBD_CLOPA	P81343 clostridium
88	2	40.0	16	1	KTRC_AREMA	P11917 arenicola m
89	2	40.0	16	1	PA21_TRIST	P82892 trimeresuru
90	2	40.0	16	1	YMOR_PSEPU	Q02210 pseudomonas
91	2	40.0	17	1	B29K_PORGI	P81784 porphyromon
92	2	40.0	17	1	BOL1_MEGPE	P10521 megabombus
93	2	40.0	17	1	BOL2_MEGPE	P07493 megabombus
94	2	40.0	17	1	BOL3_MEGPE	P07494 megabombus
95	2	40.0	17	1	BOL4_MEGPE	P07495 megabombus
96	2	40.0	17	1	BOL5_MEGPE	P07496 megabombus
97	2	40.0	17	1	RANR_RANRU	P08952 rana rugosa
98	2	40.0	17	1	SP51_BACLI	P27642 bacillus li
99	2	40.0	17	1	UP31_UPEIN	P82032 uperoleia i
100	2	40.0	17	1	UP32_UPEIN	P82033 uperoleia i

# ALIGNMENTS

## RESULT 1

### CISY\_STRHY

ID CISY\_STRHY STANDARD; PRT; 20 AA.  
AC P20903;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Citrate synthase (EC 2.3.3.1) (Fragment).  
GN GLTA.  
OS Streptomyces hygroscopicus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1912;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=SF1293;  
RX MEDLINE=90334852; PubMed=1368511;  
RA Shimotohno K.W., Imai S., Murakami T., Seto H.;  
RT "Purification and characterization of citrate synthase from  
RT Streptomyces hygroscopicus SF-1293 and comparison of its properties  
RT with those of 2-phosphinomethylmalic acid synthase.";  
RL Agric. Biol. Chem. 54:463-470(1990).  
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate +  
CC CoA.  
CC -!- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY NADH.  
CC -!- PATHWAY: Tricarboxylic acid cycle.

CC -!- SUBUNIT: Homohexamer.  
 CC -!- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS  
 CC CAPABLE OF OXIDATIVE METABOLISM.  
 CC -!- SIMILARITY: Belongs to the citrate synthase family.  
 DR PIR; PQ0046; PQ0046.  
 DR InterPro; IPR002020; Citrate\_synt.  
 DR PROSITE; PS00480; CITRATE\_SYNTHASE; PARTIAL.  
 KW Transferase; Tricarboxylic acid cycle; Allosteric enzyme.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2234 MW; C527EC7A87119597 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 6 VLR 8

## RESULT 2

### OMPW\_VIBAL

ID OMPW\_VIBAL STANDARD; PRT; 20 AA.  
 AC P83151;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Outer membrane protein W (Outer membrane protein 25Va) (Omp25Va)  
 DE (Fragment).  
 GN OMPW.  
 OS Vibrio alginolyticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=663;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=NCIMB 1903T;  
 RA Onji M., Hirabayashi J., Suzuki S.;  
 RT "Characterization of major outer membrane proteins of Vibrio  
 RT alginolyticus and the stability against proteases."  
 RL Microbes Environ. 0:0-0(2002).  
 CC -!- SUBCELLULAR LOCATION: Outer membrane.  
 CC -!- SIMILARITY: BELONGS TO THE OMPW/ALKL FAMILY.  
 KW Outer membrane.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2096 MW; D29EE7FCA16C0D37 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 7 VLR 9

## RESULT 3

PUFK\_RHOSH  
ID PUFK\_RHOSH STANDARD; PRT; 20 AA.  
AC Q53121; O08033;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Transcriptional regulatory protein pufK.  
GN PUFK.  
OS Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
OC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1063;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;  
RX MEDLINE=96349111; PubMed=8760918;  
RA Gong L., Kaplan S.;  
RT "Translational control of puf operon expression in Rhodobacter  
RT sphaeroides 2.4.1.";  
RL Microbiology 142:2057-2069(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;  
RA McGlynn P.;  
RT "R.sphaeroides genes bchC, bchX, bchY, bchZ and pufQ.";  
RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;  
RX MEDLINE=20115911; PubMed=10648776;  
RA Choudhary M., Kaplan S.;  
RT "DNA sequence analysis of the photosynthesis region of Rhodobacter  
RT sphaeroides 2.4.1.";  
RL Nucleic Acids Res. 28:862-867(2000).  
CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF PUFB.  
CC -----  
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CC -----  
DR EMBL; S82643; AAB46798.1; -.  
DR EMBL; AJ010302; CAB38751.1; -.  
DR EMBL; AF195122; AAF24301.1; -.  
DR PIR; T50757; T50757.  
KW Transcription regulation.  
SQ SEQUENCE 20 AA; 2262 MW; 764DBD64B9DD990C CRC64;

Query Match 60.0%; Score 3; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||



Db 15 VLR 17

RESULT 4

RL36\_DESDE

ID RL36\_DESDE STANDARD; PRT; 26 AA.  
AC Q46501;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 50S ribosomal protein L36 (Fragment).  
GN RPMJ.  
OS Desulfovibrio desulfuricans.  
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;  
OC Desulfovibrionaceae; Desulfovibrio.  
OX NCBI\_TaxID=876;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=G20;  
RA English R.S., Wall J.D.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE L36P FAMILY OF RIBOSOMAL PROTEINS.  
CC -----  
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CC -----  
DR EMBL; U57079; AAB01996.1; -.  
DR HSSP; P80256; 1DFE.  
DR HAMAP; MF\_00251; -; 1.  
DR InterPro; IPR000473; Ribosomal\_L36.  
DR Pfam; PF00444; Ribosomal\_L36; 1.  
DR TIGRFAMs; TIGR01022; rpmJ\_bact; 1.  
DR PROSITE; PS00828; RIBOSOMAL\_L36; PARTIAL.  
KW Ribosomal protein.  
FT NON\_TER 26 26  
SQ SEQUENCE 26 AA; 3022 MW; FB13A4590E5202D4 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
|||  
Db 22 VLR 24

RESULT 5

L52\_ADE07

ID L52\_ADE07 STANDARD; PRT; 27 AA.  
AC P05663;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Late L1 52 kDa protein (Fragment).  
 OS Human adenovirus type 7.  
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
 OX NCBI\_TaxID=10519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Gomen;  
 RX MEDLINE=83183660; PubMed=6301944;  
 RA Engler J.A., Hoppe M.S., van Bree M.P.;  
 RT "The nucleotide sequence of the genes encoded in early region 2b of  
 RT human adenovirus type 7.";   
 RL Gene 21:145-159(1983).  
 CC -!- FUNCTION: INVOLVED IN VIRION ASSEMBLY.  
 CC -----  
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 CC -----  
 DR EMBL; X03000; CAA26776.1; -.  
 DR InterPro; IPR004292; Adeno\_52K.  
 DR Pfam; PF03052; Adeno\_52K; 1.  
 KW Late protein.  
 FT NON\_TER 27 27  
 SQ SEQUENCE 27 AA; 3108 MW; E5A8288B117BB533 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 4 VLR 6

#### RESULT 6

##### COA1\_BPI22

ID COA1\_BPI22 STANDARD; PRT; 29 AA.  
 AC P15413;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Coat protein C, polypeptide I.  
 GN VII.  
 OS Bacteriophage I2-2.  
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.  
 OX NCBI\_TaxID=10869;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92211729; PubMed=1556749;  
 RA Stassen A.P., Schonmakers E.F., Yu M., Schoenmakers J.G.,  
 RA Konings R.N.H.;  
 RT "Nucleotide sequence of the genome of the filamentous bacteriophage

RT I2-2: module evolution of the filamentous phage genome.";  
 RL J. Mol. Evol. 34:141-152(1992).  
 CC -!- SUBUNIT: COAT PROTEIN C IS COMPOSED OF TWO SUBUNITS, POLYPEPTIDE I  
 CC (GENE VII) AND POLYPEPTIDE II (GENE IX).  
 CC -----  
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 CC -----  
 DR EMBL; X14336; CAA32515.1; -.  
 DR PIR; S08088; S08088.  
 KW Coat protein.  
 SQ SEQUENCE 29 AA; 2966 MW; DB7DCC3C5EDCBAD3 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLR 4  
 |||  
 Db 27 VLR 29

#### RESULT 7

##### GT\_SERMA

ID GT\_SERMA STANDARD; PRT; 31 AA.  
 AC P22416;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Glutathione S-transferase GST-7.3 (EC 2.5.1.18) (Fragment).  
 OS Serratia marcescens.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Serratia.  
 OX NCBI\_TaxID=615;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=CIP 6755;  
 RX MEDLINE=91198121; PubMed=2015287;  
 RA di Ilio C., Aceto A., Piccolomini R., Allocati N., Faraone A.,  
 RA Bucciarelli T., Barra D., Feferici G.;  
 RT "Purification and characterization of a novel glutathione transferase  
 RT from Serratia marcescens.";  
 RL Biochim. Biophys. Acta 1077:141-146(1991).  
 CC -!- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER  
 CC OF EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.  
 CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.  
 CC -!- SUBUNIT: Homodimer.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY. BETA SUBFAMILY.  
 DR PIR; S14727; S14727.  
 DR HSSP; P39100; 1A0F.  
 KW Transferase.

FT ACT\_SITE 10 10 BY SIMILARITY.  
 FT NON\_TER 31 31  
 SQ SEQUENCE 31 AA; 3434 MW; AD993D56CD9AB0D5 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 17 VLR 19

# RESULT 8

## PETL\_MESVI

ID PETL\_MESVI STANDARD; PRT; 31 AA.  
 AC Q9MUN4;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome b6-f complex subunit VI (Cytochrome b6f complex subunit  
 DE petL).  
 GN PETL.  
 OS Mesostigma viride.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae;  
 OC Mesostigmatales; Mesostigmataceae; Mesostigma.  
 OX NCBI\_TaxID=41882;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NIES-296;  
 RX MEDLINE=20150907; PubMed=10688199;  
 RA Lemieux C., Otis C., Turmel M.;  
 RT "Ancestral chloroplast genome in Mesostigma viride reveals an early  
 RT branch of green plant evolution.";  
 RL Nature 403:649-652(2000).  
 CC -!- FUNCTION: THE CYTOCHROME B6-F COMPLEX FUNCTIONS IN THE LINEAR  
 CC CROSS-MEMBRANE TRANSPORT OF ELECTRONS BETWEEN PHOTOSYSTEM II AND  
 CC I, AS WELL AS IN CYCLIC ELECTRON FLOW AROUND PHOTOSYSTEM I. PETL  
 CC IS IMPORTANT FOR PHOTOAUTOTROPHIC GROWTH AS WELL AS FOR ELECTRON  
 CC TRANSFER EFFICIENCY AND STABILITY OF THE CYTOCHROME B6-F COMPLEX  
 CC (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Thylakoid membrane-associated (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the petL family.  
 CC -----  
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 CC -----  
 DR EMBL; AF166114; AAF43866.1; -.  
 DR HAMAP; MF\_00433; -; 1.  
 DR Pfam; PF05115; PetL; 1.

KW Electron transport; Chloroplast; Respiratory chain; Transmembrane;  
 KW Thylakoid.  
 FT TRANSMEM 4 24 POTENTIAL.  
 SQ SEQUENCE 31 AA; 3397 MW; 5BF71DAF8A8B9743 CRC64;

Query Match 60.0%; Score 3; DB 1; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLR 4  
 |||  
 Db 24 VLR 26

# RESULT 9

## ACPH\_RABIT

ID ACPH\_RABIT STANDARD; PRT; 6 AA.  
 AC P25154;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)  
 DE (APH) (Acylaminoacyl-peptidase) (Fragment).  
 GN APEH.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Muscle;  
 RX MEDLINE=92222120; PubMed=1807161;  
 RA Krishna R.G., Chin C.C.Q., Wold F.;  
 RT "N-terminal sequence analysis of N alpha-acetylated proteins after  
 RT unblocking with N-acylaminoacyl-peptide hydrolase.";  
 RL Anal. Biochem. 199:45-50(1991).  
 CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-  
 CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE  
 CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.  
 CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.  
 CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid  
 CC + peptide.  
 CC -!- SUBUNIT: Homotetramer.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.  
 DR PIR; A49792; A49792.  
 DR MEROPS; S09.004; -.  
 DR InterPro; IPR002471; Prol\_endopep\_ser.  
 DR PROSITE; PS00708; PRO\_ENDOPEP\_SER; PARTIAL.  
 KW Hydrolase; Acetylation.  
 FT MOD\_RES 1 1 ACETYLATION.  
 FT NON\_TER 6 6  
 SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
||  
Db 5 VL 6

RESULT 10

CARP\_MYTED

ID CARP\_MYTED STANDARD; PRT; 7 AA.  
AC P10420;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 01-MAR-1989 (Rel. 10, Last annotation update)  
DE Catch-relaxing peptide (CARP).  
OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;  
OC Mytiloidea; Mytilidae; Mytilus.  
OX NCBI\_TaxID=6550;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=88052022; PubMed=3676797;  
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,  
RA Muneoka Y.;  
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";  
RL Brain Res. 422:374-376(1987).  
CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)  
CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS  
CC RETRACTOR MUSCLE.  
DR PIR; A29342; ECMUCR.  
KW Hormone; Amidation.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 5 LR 6

RESULT 11

FAR1\_HELTI

ID FAR1\_HELTI STANDARD; PRT; 7 AA.  
AC P41871;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide GDPFLRF-amide.  
OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC Lymnaeidae; Planorbidae; Helisoma.  
OX NCBI\_TaxID=27815;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428;

RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, *Helisoma*  
 RT *trivolvis*.";  
 RL Peptides 15:31-36(1994).  
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING  
 CC THE KIDNEY, MANTLE AND SKIN.  
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 5 LR 6

#### RESULT 12

##### FAR1\_MACRS

ID FAR1\_MACRS STANDARD; PRT; 7 AA.  
 AC P83274;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP1 (DRNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,  
 RA Sithigorngul W.;  
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn *Macrobrachium rosenbergii*.";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -!- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||

Db 5 LR 6

RESULT 13

FAR1\_PROCL

ID FAR1\_PROCL STANDARD; PRT; 7 AA.  
AC P38499;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Cardioexcitatory FMRFamide homolog NF1.  
OS Procambarus clarkii (Red swamp crayfish).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Astacoidea; Cambaridae; Procambarus.  
OX NCBI\_TaxID=6728;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pericardial organs;  
RX MEDLINE=93248032; PubMed=8387183;  
RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;  
RT "Isolation of two FMRFamide-related peptides from crayfish  
RT pericardial organs."  
RL Peptides 14:137-143(1993).  
CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 5 LR 6

RESULT 14

FAR2\_ASCSU

ID FAR2\_ASCSU STANDARD; PRT; 7 AA.  
AC P31890;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE FMRFamide-like neuropeptide AF2.  
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
OC Ascarididae; Ascaris.  
OX NCBI\_TaxID=6253, 6233;  
RN [1]  
RP SEQUENCE.



RC SPECIES=A.suum;  
 RX MEDLINE=93324431; PubMed=8332542;  
 RA Cowden C., Stretton A.O.W.;  
 RT "AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";  
 RL Peptides 14:423-430(1993).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=P.redivivus;  
 RX MEDLINE=95060998; PubMed=7970891;  
 RA Maule A.G., Shaw C., Bowman J.W.;  
 RT "The FMRFamide-like neuropeptide AF2 (Ascaris suum) is present in the  
 RT free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida).";  
 RL Parasitology 109:351-356(1994).  
 CC -!- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.  
 CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF  
 CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 5 LR 6

# RESULT 15

## FAR2\_PROCL

ID FAR2\_PROCL STANDARD; PRT; 7 AA.  
 AC P38498;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Cardioexcitatory FMRFamide homolog DF2.  
 OS Procambarus clarkii (Red swamp crayfish).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Astacoidea; Cambaridae; Procambarus.  
 OX NCBI\_TaxID=6728;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=93248032; PubMed=8387183;  
 RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;  
 RT "Isolation of two FMRFamide-related peptides from crayfish  
 RT pericardial organs.";  
 RL Peptides 14:137-143(1993).  
 CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
 CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
 CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.

KW Neuropeptide; Amidation.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 5 LR 6

RESULT 16

CAD1\_ENTFA

ID CAD1\_ENTFA STANDARD; PRT; 8 AA.  
AC P13268;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CAD1.  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=85051889; PubMed=6437872;  
RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
RA Craig R.A., Clewell D.B., Suzuki A.;  
RT "Isolation and structure of the bacterial sex pheromone, cAD1, that  
RT induces plasmid transfer in Streptococcus faecalis.";  
RL FEBS Lett. 178:97-100(1984).  
CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
CC HEMOLYSIN PLASMID PAD1.  
KW Pheromone.  
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
||  
Db 5 VL 6

RESULT 17

COW2\_CONPU

ID COW2\_CONPU STANDARD; PRT; 8 AA.  
AC P58785;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leu-contryphan-P.  
OS Conus purpurascens (Purple cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=41690;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC STRAIN=Clipperton Island; TISSUE=Venom;  
 RX MEDLINE=99388839; PubMed=10461743;  
 RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
 RA Olivera B.M.;  
 RT "A novel D-leucine-containing Conus peptide: diverse conformational  
 RT dynamics in the contryphan family.";  
 RL J. Pept. Res. 54:93-99(1999).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.  
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.  
 KW Toxin; Hydroxylation; D-amino acid.  
 FT DISULFID 2 8  
 FT MOD\_RES 4 4 D-LEUCINE.  
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
 ||  
 Db 3 VL 4

#### RESULT 18

##### FAR1\_PANRE

ID FAR1\_PANRE STANDARD; PRT; 8 AA.  
 AC P41872;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide PF1 (SDPNFLRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93027659; PubMed=1408999;  
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
 RA Garrison R.D., Williams J.F., Friedman A.R.;  
 RT "Two FMRFamide-like peptides from the free-living nematode  
 RT Panagrellus redivivus.";  
 RL Peptides 13:209-214(1992).  
 CC -!- FUNCTION: MYOACTIVE.  
 CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
 CC CAUDALLY TO THE BASE OF THE PHARYNX.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 6 LR 7

RESULT 19

FAR1\_PENMO

ID FAR1\_PENMO STANDARD; PRT; 8 AA.  
AC P83316;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP1 (GDRNFLRF-amide).  
OS Penaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
RT of the giant tiger prawn Penaeus monodon.";  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AA8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 6 LR 7

RESULT 20

FAR2\_MACRS

ID FAR2\_MACRS STANDARD; PRT; 8 AA.  
AC P83275;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP2 (ADKNFLRF-amide).

OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,  
 RA Sithigorngul W.;  
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -!- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 6 LR 7

# RESULT 21

## FAR3\_HOMAM

ID FAR3\_HOMAM STANDARD; PRT; 8 AA.  
 AC P41486;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE FMRFamide-like neuropeptide 3 (FLI 3) (F2).  
 OS Homarus americanus (American lobster).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Nephropoidea; Nephropidae; Homarus.  
 OX NCBI\_TaxID=6706;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pericardial organs;  
 RX MEDLINE=88116164; PubMed=3429714;  
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;  
 RT "Purification and characterization of FMRFamidelike immunoreactive  
 RT substances from the lobster nervous system: isolation and sequence  
 RT analysis of two closely related peptides.";  
 RL J. Comp. Neurol. 266:16-26(1987).  
 CC -!- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 MM  
 CC POTASSIUM IN THE PRESENCE OF CALCIUM.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.

FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 6 LR 7

#### RESULT 22

##### FAR4\_HOMAM

ID FAR4\_HOMAM STANDARD; PRT; 8 AA.  
AC P41487;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide 4 (FLI 4) (F1).  
OS Homarus americanus (American lobster).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Nephropoidea; Nephropidae; Homarus.  
OX NCBI\_TaxID=6706;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pericardial organs;  
RX MEDLINE=88116164; PubMed=3429714;  
RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;  
RT "Purification and characterization of FMRFamidelike immunoreactive  
RT substances from the lobster nervous system: isolation and sequence  
RT analysis of two closely related peptides.";  
RL J. Comp. Neurol. 266:16-26(1987).  
CC -!- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC  
CC NEUROMUSCULAR JUNCTIONS.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 6 LR 7

#### RESULT 23

##### FAR4\_MACRS

ID FAR4\_MACRS STANDARD; PRT; 8 AA.  
AC P83277;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP4 (APALRLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,  
 RA Sithigorngul W.;  
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -!- MASS SPECTROMETRY: MW=943; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 943 MW; 9CD40734072DC76D CRC64;  
  
 Query Match 40.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LR 4  
 ||  
 Db 4 LR 5

RESULT 24  
 BS43\_SERPL  
 ID BS43\_SERPL STANDARD; PRT; 9 AA.  
 AC P83375;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bacteriocin serracin P 43 kDa subunit (Fragment).  
 OS Serratia plymuthica.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Serratia.  
 OX NCBI\_TaxID=82996;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC STRAIN=J7;  
 RX MEDLINE=22293561; PubMed=12406768;  
 RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,  
 RA Van Beeumen J., Thonart P.;  
 RT "Characterization of serracin P, a phage-tail-like bacteriocin, and  
 RT its activity against Erwinia amylovora, the fire blight pathogen.";  
 RL Appl. Environ. Microbiol. 68:5704-5710(2002).  
 CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).  
 CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium  
 CC E. amylovora.  
 DR InterPro; IPR006498; Tail\_tube.

DR Pfam; PF04985; Phage\_tube; 1.  
KW Antibiotic; Bacteriocin.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1095 MW; 1E66D412C871E1FB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
||  
Db 8 VL 9

#### RESULT 25

##### FAR2\_PANRE

ID FAR2\_PANRE STANDARD; PRT; 9 AA.  
AC P41873;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide PF2 (SADPNFLRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93027659; PubMed=1408999;  
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
RA Garrison R.D., Williams J.F., Friedman A.R.;  
RT "Two FMRFamide-like peptides from the free-living nematode  
RT Panagrellus redivivus.";  
RL Peptides 13:209-214(1992).  
CC -!- FUNCTION: MYOACTIVE.  
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
CC CAUDALLY TO THE BASE OF THE PHARYNX.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 7 LR 8

#### RESULT 26

##### FAR3\_MACRS

ID FAR3\_MACRS STANDARD; PRT; 9 AA.  
AC P83276;  
DT 28-FEB-2003 (Rel. 41, Created)



DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP3 (NYDKNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,  
 RA Sithigorngul W.;  
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -!- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1216 MW; 18220729C4433ABB CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 7 LR 8

#### RESULT 27

##### FAR3\_PENMO

ID FAR3\_PENMO STANDARD; PRT; 9 AA.  
 AC P83318;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP3 (AQPSMRLRF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn Penaeus monodon.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1121.2; METHOD=MALDI.

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1105 MW; CCD107340685A776 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 7 LR 8

#### RESULT 28

FAR4\_PENMO

ID FAR4\_PENMO STANDARD; PRT; 9 AA.  
AC P83319;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide FLP4 (SQPSMRLRF-amide).  
OS Penaeus monodon (Penoeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
RT of the giant tiger prawn Penaeus monodon."  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 7 LR 8

#### RESULT 29

FAR5\_PENMO

ID FAR5\_PENMO STANDARD; PRT; 9 AA.

AC P83320;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP5 (SMPSLRLRF-amide).  
 OS *Penaeus monodon* (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; *Penaeus*.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn *Penaeus monodon*.";  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 5 LR 6

# RESULT 30

## FAR6\_MACRS

ID FAR6\_MACRS STANDARD; PRT; 9 AA.  
 AC P83279;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP6 (DGGRNFLRF-amide).  
 OS *Macrobrachium rosenbergii* (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; *Macrobrachium*.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21107394; PubMed=11179812;  
 RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,  
 RA Sithigorngul W., Petsom A.;  
 RT "Three more novel FMRFamide-like neuropeptide sequences from the  
 RT eyestalk of the giant freshwater prawn *Macrobrachium rosenbergii*.";

RL Peptides 22:191-197(2001).  
 CC -!- MASS SPECTROMETRY: MW=1080.7; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1081 MW; 26800729C4540878 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 7 LR 8

# RESULT 31

## FAR8\_MACRS

ID FAR8\_MACRS STANDARD; PRT; 9 AA.  
 AC P83281;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP8 (VSHNNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21107394; PubMed=11179812;  
 RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,  
 RA Sithigorngul W., Petsom A.;  
 RT "Three more novel FMRFamide-like neuropeptide sequences from the  
 RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii."  
 RL Peptides 22:191-197(2001).  
 CC -!- MASS SPECTROMETRY: MW=1133.8; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 1133 MW; 845A0729C44441F5 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 7 LR 8

# RESULT 32

FAR9\_ASCSU

ID FAR9\_ASCSU STANDARD; PRT; 9 AA.  
AC P43172;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE FMRFamide-like neuropeptide AF9.  
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
OC Ascarididae; Ascaris.  
OX NCBI\_TaxID=6253;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95380362; PubMed=7651904;  
RA Cowden C., Stretton A.O.W.;  
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode  
RT Ascaris suum."  
RL Peptides 16:491-500(1995).  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LR 4  
||  
Db 7 LR 8

# RESULT 33

FARP\_CALSI

ID FARP\_CALSI STANDARD; PRT; 9 AA.  
AC P38495;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide.  
OS Callinectes sapidus (Blue crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidea; Portunidae; Callinectes.  
OX NCBI\_TaxID=6763;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92270479; PubMed=1815216;  
RA Krajniak K.G.;  
RT "The identification and structure-activity relations of a  
RT cardioactive FMRFamide-related peptide from the blue crab Callinectes  
RT sapidus."  
RL Peptides 12:1295-1302(1991).  
CC -!- FUNCTION: CARDIOACTIVE PEPTIDE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 9 9 AMIDATION.  
SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 7 LR 8

RESULT 34

FIBB\_ERYPA

ID FIBB\_ERYPA STANDARD; PRT; 9 AA.  
AC P19346;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Erythrocebus patas (Red guenon) (Hussar).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Erythrocebus.  
OX NCBI\_TaxID=9538;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=85289140; PubMed=3928610;  
RA Nakamura S., Takenaka O., Takahashi K.;  
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and  
RT patas monkey (Erythrocebus patas): their amino acid sequences,  
RT restricted mutations, and a molecular phylogeny for macaques,  
RT guenons, and baboons.";  
RL J. Biochem. 97:1487-1492(1985).  
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR PIR; D24180; D24180.  
DR InterPro; IPR002181; Fibrinogen\_C.  
DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
||  
Db 4 VL 5

RESULT 35

BRK\_ONCMY

ID BRK\_ONCMY STANDARD; PRT; 10 AA.  
AC Q9PRZ1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lysyl-bradykinin-like.  
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=8022;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94039817; PubMed=8224232;  
RA Conlon J.M., Olson K.R.;  
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from  
RT trout plasma."  
RL FEBS Lett. 334:75-78(1993).  
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR  
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Plasma.  
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.  
DR PIR; S39030; S39030.  
KW Bradykinin; Vasodilator.  
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 9 LR 10

RESULT 36

ESL\_LACCA

ID ESL\_LACCA STANDARD; PRT; 10 AA.  
AC P81758;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Putative esterase/lipase (EC 3.1.-.-) (Fragment).  
OS Lactobacillus casei.  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=1582;  
RN [1]

RP SEQUENCE.  
 RC STRAIN=IFPL731;  
 RA Lopez de Felipe F.;  
 RL Submitted (MAR-1999) to the SWISS-PROT data bank.  
 KW Hydrolase; Serine esterase.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
 ||  
 Db 6 VL 7

# RESULT 37

## FAR2\_PENMO

ID FAR2\_PENMO STANDARD; PRT; 10 AA.  
 AC P83317;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP2 (AYSNLNYLRF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn Penaeus monodon."  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1260.0; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1260 MW; 88F9023B54472455 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 8 LR 9

# RESULT 38



## FAR5\_MACRS

ID FAR5\_MACRS STANDARD; PRT; 10 AA.  
 AC P83278;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP5 (DRTPALRLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RA Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,  
 RA Sithigorngul W.;  
 RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
 RT freshwater prawn Macrobrachium rosenbergii.";  
 RL Comp. Biochem. Physiol. 120B:587-595(1998).  
 CC -!- MASS SPECTROMETRY: MW=1243.4; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1244 MW; 9A1A5334072DC771 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 6 LR 7

## RESULT 39

## FAR7\_MACRS

ID FAR7\_MACRS STANDARD; PRT; 10 AA.  
 AC P83280;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP7 (GYGDRNFLRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21107394; PubMed=11179812;  
 RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,  
 RA Sithigorngul W., Petsom A.;  
 RT "Three more novel FMRFamide-like neuropeptide sequences from the

RT eyestalk of the giant freshwater prawn *Macrobrachium rosenbergii*.  
 RL Peptides 22:191-197(2001).  
 CC -!- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540AA8 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 8 LR 9

#### RESULT 40

##### FARP\_LOCFMI

ID FARP\_LOCFMI STANDARD; PRT; 10 AA.  
 AC P38553;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE SchistoFLRFamide (PDVDHFLRF-amide) (Cardioexcitatory neuropeptide).  
 OS Locusta migratoria (Migratory locust), and  
 OS Schistocerca gregaria (Desert locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004, 7010;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=L.migratoria; TISSUE=Brain;  
 RX MEDLINE=93324430; PubMed=7687352;  
 RA Schoofs L., Holman G.M., Paemen L., Veelaert D., Amelinckx M.,  
 RA de Loof A.;  
 RT "Isolation, identification, and synthesis of PDVDHFLRFamide  
 RT (SchistoFLRFamide) in Locusta migratoria and its association with the  
 RT male accessory glands, the salivary glands, the heart, and the  
 RT oviduct.";  
 RL Peptides 14:409-421(1993).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;  
 RX MEDLINE=89246543; PubMed=2719702;  
 RA Robb S., Packman L.C., Evans P.D.;  
 RT "Isolation, primary structure and bioactivity of schistoflrf-amide, a  
 RT FMRF-amide-like neuropeptide from the locust, Schistocerca  
 RT gregaria.";  
 RL Biochem. Biophys. Res. Commun. 160:850-856(1989).  
 CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL  
 CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND  
 CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.  
 CC -!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,

CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; A32543; A32543.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||  
Db 8 LR 9

#### RESULT 41

##### FARP\_MANSE

ID FARP\_MANSE STANDARD; PRT; 10 AA.  
AC P18523;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide.  
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;  
OC Sphingidae; Sphinginae; Manduca.  
OX NCBI\_TaxID=7130;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91045350; PubMed=2235684;  
RA Kingan T.G., Teplow D.B., Phillips J.M., Riehm J.P., Rao K.R.,  
RA Hildebrand J.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,  
RA Hunt D.F.;  
RT "A new peptide in the FMRFamide family isolated from the CNS of the  
RT hawkmoth, Manduca sexta.";  
RL Peptides 11:849-856(1990).  
CC -!- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN  
CC THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL  
CC MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING  
CC FLIGHT BEHAVIOR PATTERNS.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; A43977; A43977.  
KW Amidation; Neuropeptide; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1247 MW; D3C45229D5B1F2D2 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
||

Db

8 LR 9

RESULT 42

LCMS\_LEUMA

ID LCMS\_LEUMA STANDARD; PRT; 10 AA.  
AC P21144; P41497;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leucomyosuppressin (LMS) (LeM-MS).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Head;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure and synthesis of leucomyosuppressin,  
RT an insect neuropeptide that inhibits spontaneous contractions of the  
RT cockroach hindgut.";  
RL Comp. Biochem. Physiol. 85C:329-333(1986).  
CC -!- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH  
CC PROTODEUM (HINDGUT).  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1275 MW; D3C45229D2C1EAB2 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4

||

Db 8 LR 9

RESULT 43

PORB\_METTM

ID PORB\_METTM STANDARD; PRT; 10 AA.  
AC P80901;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase  
DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)  
DE (Fragment).  
GN PORB.  
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=79929;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=97261844; PubMed=9108258;  
 RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;  
 RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases  
 RT in Methanobacterium thermoautotrophicum.";  
 RL Eur. J. Biochem. 244:862-868(1997).  
 CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-  
 CC CoA + CO(2) + reduced ferredoxin.  
 CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE  
 CC GAMMA CHAIN.  
 CC -!- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature  
 CC of 80 degrees Celsius.  
 KW Oxidoreductase.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||  
 Db 9 LR 10

#### RESULT 44

TKU1\_UREUN

ID TKU1\_UREUN STANDARD; PRT; 10 AA.  
 AC P40751;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Urechistachykinin I.  
 OS Urechis unicinctus.  
 OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.  
 OX NCBI\_TaxID=6432;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC TISSUE=Ventral nerve cord;  
 RX MEDLINE=93236558; PubMed=8476410;  
 RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;  
 RT "Two novel tachykinin-related neuropeptides in the echiuroid worm,  
 RT Urechis unicinctus.";  
 RL Biochem. Biophys. Res. Commun. 192:1-6(1993).  
 CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL  
 CC MUSCLE OF THE ANIMAL.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1177 MW; C6D1C462C9D6C5A6 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LR 4  
 ||

Db 1 LR 2

RESULT 45

UPA5\_HUMAN

ID UPA5\_HUMAN STANDARD; PRT; 10 AA.  
AC P30091;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.  
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF  
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT  
CC PROTEIN.  
DR SWISS-2DPAGE; P30091; HUMAN.  
FT NON\_TER 1 1  
FT VARIANT 9 9 G -> Y.  
FT /FTid=VAR\_000002.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VL 3  
||  
Db 6 VL 7

RESULT 46

ES1\_RAT

ID ES1\_RAT STANDARD; PRT; 11 AA.  
AC P56571;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE ES1 protein, mitochondrial (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;

RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN  
 CC (SPOT P2) IS: 8.9, ITS MW IS: 25 kDa.  
 CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.  
 KW Mitochondrion.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
 ||  
 Db 7 VL 8

#### RESULT 47

##### FAR6\_PENMO

ID FAR6\_PENMO STANDARD; PRT; 11 AA.  
 AC P83321;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Eyestalk;  
 RX MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,  
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn *Penaeus monodon*."  
 RL Comp. Biochem. Physiol. 131B:325-337(2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 11 11 AMIDATION.  
 SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy            3 LR 4  
             ||  
Db            7 LR 8

RESULT 48

RR16\_GINBI

ID    RR16\_GINBI            STANDARD;            PRT;       12 AA.  
AC    P36207;  
DT    01-JUN-1994 (Rel. 29, Created)  
DT    01-JUN-1994 (Rel. 29, Last sequence update)  
DT    28-FEB-2003 (Rel. 41, Last annotation update)  
DE    Chloroplast 30S ribosomal protein S16 (Fragment).  
GN    RPS16.  
OS    Ginkgo biloba (Ginkgo).  
OG    Chloroplast.  
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC    Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.  
OX    NCBI\_TaxID=3311;  
RN    [1]  
RP    SEQUENCE FROM N.A.  
RX    MEDLINE=95094313; PubMed=8001171;  
RA    Richard M., Tremblay C., Bellemare G.;  
RT    "Chloroplastic genomes of Ginkgo biloba and Chlamydomonas moewusii  
RT    contain a chlB gene encoding one subunit of a light-independent  
RT    protochlorophyllide reductase.";  
RL    Curr. Genet. 26:159-165(1994).  
CC    -!- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.  
CC    -----  
CC    This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC    or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC    -----  
DR    EMBL; U01531; AAA66977.1; -.  
DR    HAMAP; MF\_00385; -; 1.  
DR    InterPro; IPR000307; Ribosomal\_S16.  
DR    PROSITE; PS00732; RIBOSOMAL\_S16; 1.  
KW    Ribosomal protein; Chloroplast.  
FT    NON\_TER            12       12  
SQ    SEQUENCE    12 AA;    1488 MW;    6700EDAF9D033734 CRC64;

Query Match                    40.0%;    Score 2;    DB 1;    Length 12;  
Best Local Similarity    100.0%;    Pred. No. 3.8e+03;  
Matches       2;    Conservative       0;    Mismatches       0;    Indels       0;    Gaps       0;

Qy            3 LR 4  
             ||  
Db            4 LR 5

RESULT 49

TM2A\_METMA

ID    TM2A\_METMA            STANDARD;            PRT;       12 AA.



AC P80652;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit  
 DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin--coenzyme M  
 DE methyltransferase 28 kDa subunit) (Fragment).  
 OS Methanosarcina mazei (Methanosarcina frisia).  
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;  
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2209;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;  
 RX MEDLINE=96370840; PubMed=8774736;  
 RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;  
 RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:  
 RT coenzyme M methyltransferase from Methanosarcina mazei Go1  
 RT reconstituted in ether lipid liposomes.";  
 RL Eur. J. Biochem. 239:857-864(1996).  
 CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN  
 CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND  
 CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-  
 CC TETRAHYDROMETHANOPTERIN.  
 CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-  
 CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-  
 CC (methylthio)ethanesulfonate.  
 CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 40.0%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VL 3  
 ||  
 Db 7 VL 8

# RESULT 50

## CRBL\_VESCR

ID CRBL\_VESCR STANDARD; PRT; 13 AA.  
 AC P01518;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Crabrolin.  
 OS Vespa crabro (European hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID=7445;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Venom;  
 RX MEDLINE=84289390; PubMed=6206053;  
 RA Argiolas A., Pisano J.J.;  
 RT "Isolation and characterization of two new peptides, mastoparan C and  
 RT crabrolin, from the venom of the European hornet, Vespa crabro.";  
 RL J. Biol. Chem. 259:10106-10111(1984).  
 RN [2]  
 RP SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.  
 RX MEDLINE=97419326; PubMed=9273892;  
 RA Krishnakumari V., Nagaraj R.;  
 RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue  
 RT peptide from the venom of the European hornet, Vespa crabro, and its  
 RT analogs.";  
 RL J. Pept. Res. 50:88-93(1997).  
 CC -!- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 CC of neutrophils. Has antimicrobial and hemolytic activity.  
 DR PIR; A01781; JZVHP1.  
 KW Mast cell degranulation; Chemotaxis; Amidation; Antibiotic.  
 FT MOD\_RES 13 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1497 MW; 515EF8FCEA8D2407 CRC64;

Query Match 40.0%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LR 4  
 ||  
 Db 6 LR 7

Search completed: November 28, 2003, 15:39:51  
 Job time : 12 secs